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U12314 Cenchrus ci AP005613 Oryza sat AP005991 Oryza sat

Description

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Cenchrus ciliaris

Cenchrus ciliaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Paniceae; Cenchrus.

1 (bases 1 to 1335)
                                                                                               Cenchrus ciliaris clone PX7 peroxidase mRNA, complete cds. U12314 U12314.1 GI:520567
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                               Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DNA, clone:OSJNBa0082C09
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Thesis (1994) Botany,
2 (bases 1 to 1335)
      Sasaki, T., Matsumoto, T. and Katayose, Y
                              Published Only in Database (2002)
2 (bases 1 to 160562)
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KNVERACPGVVSCATIVELAARBGENLLGGFWNVPLGRRDSTTAMUSLAKQNLEPPT
SLGTLISLEGGRLSARDMIALSGAHRAQARCTFERGRIYGDTNIDASFAALQQTCPR
SGGDCNLAPIDAQTPARFDNAYYTNLVSRRGLFHSDQELFNGGSQDALVRQYSSSPSQ
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/protein_id="AAA20472.1"
/db_xref="G1:520568"
/translation="MAAPTLMQCLLAISLLSETAHAQLSTTFYASSCPNLQTVVRAAM
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/clone_lib="lambda gt-10"
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Direct Submission

Direct Submission

Submitted (01-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias affrc go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs daps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This is a 'working draft' sequence.

* This sequence will be replaced by the finished sequence as soon as it is available and the replaced by the finished sequence as soon as it is available and the replaced to the finished sequence as soon as it is available and the replaced to the finished sequence as soon as it is available and the replaced to the sequence as soon as it is available and the sequence as soon as it is available and the sequence as soon as it is available and the sequence as soon as it is available and the sequence as soon as it is available and the sequence as soon as it is available.
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Submitted (01-AUG-2002) Takuji Sasaki, National Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           published Only in Database (2001)
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/chromosome="2"
/clone="0SJNBa0082C09"
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                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.cseries: IRAL Plate: 21 Row: h Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by The I.M.A.G.B. Consorthim (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens, ubiquitin-conjugating enzyme E2D 1 (homologous to yeast UBC4/5), clone MGC:14673 IMAGE:4106710, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                      Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
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Similarity 100.0%;
34; Conservative 0;
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/cultivar="Nipponbare"
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/chromosome="2"
            /product="ubiquitin-conjugating enzyme E2D to yeast UBC4/5)"
                                                                                                             /db_xref="LocusID:7321"
/db_xref="taxon:9606"
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/clone_type="Bone marrow, acute
/clone_lib="NHH_MGC_55"
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33053 c 33283 g
                                                                                                  /lab_host="DH10B"
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/protein_id="AAH05980.1"
                                                /codon_start=1
                                                                                /note="Vector:
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(Dickson, Mark) mcd@paxil.stanford.edu
4., Schmutz, J., Grimwood, J., Rodrique
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9334 TTCAACGGCGGGTCGCAGGACGCGCTGGTGAGG 9302
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                                                  TTCAACGGCGGGTCGCAGGACGCGCTGGTGAGG 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakidabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the Fleces is believed to be correct as given, however the sizes of the Japs between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draff' sequence.
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2 (bases 1 to 135792)
3 saski, T., Matsumoto, T. and Yamamoto, K. Direct Submission
Submitter's C.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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*** SEQUENCING IN PROGRESS ***, in ordered pieces.
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the accession number will be preserved.
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LLSICSLLCDPNPDDPLVPDIAQIYKSDKEKYNRHAREWTQKYAM"
a 311 c 261 g 463 t
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30304 c 30206
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/chromosome="6"
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a valiable and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.
                                     1 (bases 1 to 950)
Weng, C.K. and To, K.Y.
                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                              Lycopersicon esculentum
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                 Molecular characterization
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                                                                                        Direct Submission
Submitted (30-DEC-1999) Genome
University School of Medicine,
MO 63108, USA
                                                                                                                                                                              2 (bases 1 to 186896)

Tomlinson,C., Dixon,R., Kozlowicz,A. and Boyer,E. The sequence of Homo sapiens BAC clone RP11-121A1 (uppublished (2001)
           Direct Submission
Submitted (19-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens BAC clone
AC019057
AC019057.8 GI:15668119
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                                                             Waterston, R.H.
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                                                                                                                                                       Waterston, R.H.
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                                                                                                                                                                                                                                                                                                           1 (bases 1 to 186896)
Sulston, J.E. and Waterston, R.
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USA
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Data from AC092170 and AC064870 was used to finish this clone, AC019057. Polymorphisms exist between RP11-121A1, RP11-814G20, and RP11-575E20. EXAMPLES RP11-575E20. LOCALION/QUALIFIERS 1. 186896 1. 186896 2. 1. 186896 2. 2. 1. 186896 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc SOURCE INFORMATION: The RRCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell park Cancer Institute (http://bacpac.med.buffalo.edu) VECTOR: pBACe3.6 NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-814G2O; the clone sequenced to the right is RP11-175PEDO, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-121A1; actual end is at base	AUTHORS TITLE Direct Submission TITLE Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA COMMENT COMMENT CONTROL On Sep 19, 2001 this sequence version replaced gi:15144336. CONTROL Center: Washington University Genome Sequencing Center Center code: WIGGS Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu
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Submisted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdnaldims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology CDNA library
construction, 5'- 6 3'-end one pass sequencing: Departent of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                        Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujiwara,T., Ono,T., Yamada,K., Fujiki,Y., Ozaki,K., Hirao,M., Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligo capping; fis (full insert sequence).
Homo sapiens primary endothelial cells of human umbilical vein cDNA, to mRAA, clone_lib:HUV clone:HUV00250.
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32; Conser
                                                                                                                                                                                                                                                                                                           Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK026389 1253 bp mRNA linear PRI 29-SEP-2000 Homo sapiens cDNA: FLJ22736 fis, clone HUV00250, highly similar to AF131821 Homo sapiens clone 24877 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                    NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/rpt_family="(TTTTTG)n"
25161. .26212
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                                                       Location/Qualifiers
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29550. .29843
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29272. .29416
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100.0%; Pred. No. 6.3e-06;
ive 0; Mismatches 0;
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polyA_site
count 38
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                                                                                                                                                                         TTTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequenced by Qiagen (Hilden/Germany) within the 2DNA sequencing consortium of the German Genome Project.
This clone (DKFZP666M0979) is available at the R2PD in Berlin. Please contact the R2PD: Ressourcenzentrum, Heubherweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.dc.Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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Homo sapiens mRNA; cDNA DKFZp686M0979 (from
AL833641 GI:21734288
                                                                                                                                                                                                                    31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1495)
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/fissue_type="cDNA-collection"
/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sf1; host DH10B; sites Sf1A + Sf1IB"
/dev_stage="adult"
1422. 1427
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/note="cloning vector pME18SFL3"
1. .1253
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/cell_type="primary endothelial cells of human umbilical
vein"
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/db_xref="taxon:9606"
1844 bp
from Patent WO0073348
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100.0%; Pred. No. 1.2e-
tive 0; Mismatches
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KEYWORDS
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AX089940
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1844)

Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Tumas,D.,

Watanabe,C.K. and Wood,W.I.

Compositions and methods for the treatment of immune related
                                                                                                       1844 bp
Sequence 175 from Patent W00208284.
XX454590
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1 (bases 1 to 1844)

Baker, K. P., Goddard, A., Gurney, A. L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D. L., Smith, V., Watanabe, C. K. and Wood, W. I. Methods and compositions for inhibiting neoplastic cell growth Methods and Compositions for inhibiting neoplastic cell growth Patent: WO 0073348 A 23 07-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech,
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: WO 0116319-A 1 08-MAR-2001; Genentech, Inc. (US)
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/db_xref="taxon:9606"
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RESULT 15 AX491068 LOCUS DEFINITION ACCESSION VERSION	Best Local Matches 3 Qy 1324 TTT Db 1787 TTT	JOURNAL SOURCE SOURCE BASE COUNT ORIGIN	REFERENCE AUTHORS	RESULT 14 AX464342 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	es 24 87	ORIGIN Query Matc Best Local	FEATURES Source	TITLE	REFERENCE AUTHORS
AX491068 1844 bp DNA linear PAT 16-AUG-2002 V Sequence 175 from Patent WOO200690. AX491068 AX491068.1 GI:22323871	DOCAL Similarity 100.0%; Pred. No. 12e-05; Socal Similarity 100.0%; Pred. No. 12e-05; S 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0; TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	atent: WO 0140466-A 475 07-JUN-2001; enentech Inc. (US) Location/Qualifiers 1. 1844 /organism="Homo sapiens" /db_xref="taxon:9606" 398 a 564 c 590 g 292 t	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.C., Gerritsen, M.E., Goddward, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tunas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z. Secreted and transmembrane polypeptides and nucleic acids encoding same	AX464342 1844 bp DNA Sequence 475 from Patent WOO140466. AX464342 AX464342.1 GI:21899187 human.	31; Conservative 0; Mismatches 0 TTCGGAAAAAAAAAAAAAAAAAAAAAAAAAAA 1354 	398 a 564 c 590 g 292 t tch 2.3%; Score 31; DB 6; Length 1844; al Similarity 100.0%; Pred. No. 1.2e-05;	I. (US) Location/Qualifiers e 11844 /organism="Homo sapiens" /db_xref="taxon:9606"	J., Gurney, A.L., Hillan, K.J., Marsters, Stephan, J.P., Watanabe, C.K., Williams, February, Stephan, J.P., Watanabe, C.K., Williams, February, And Translation of the diagnosis of	Gerber,H., Gerritsen,M.E.,

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KEYWORDS
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Search completed: May 3, 2003, 11:14:25 Job time: 3317 secs
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source
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                                                                                  Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis patent: WO 0200690-A 175 03-JAN-2002; Genentech, Inc. (US)
Location/Qualifiers
1. 1844
/organism-"Homo sapiens"
/db_xref="taxon:9606"
398 a 564 c 590 g 292 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
Homo spiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Goddwski,P.J., Gurney,A.L., Hillan,K.J., MarSters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.
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Post-processing: Listing first 45 summaries

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Total number of

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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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specification or its complement.
(a) assessing whether a patient i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer in a patient;
(d) assessing the efficacy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV14239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001.
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                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                       Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                 (MILL-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer is assessing the prostate cell carcinogenic potential of a determining whether prostate cancer has metastasized in assessing the aggressiveness or indolence of prostate cancers.
                                                                                                                                                                                                                                                              2001-662795/76.
                                                                                                                         ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate
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32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also useful as a pharmacodyanamic or
                                                                                                                                                                                                                                                                                                                                                 MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369
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                                                                                                                                                                                                                                                                                                                                                                                          2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-183319P
2000US-189862P
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                                                                                                                         2374; 11750pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression marker cDNA 14230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 0%;
                                                                                                                                                                                                                                                                                                          Monahan JE;
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in Tables 1-9 (ABV00010-ABV62213)
nent. (I) is useful for:
lent is afflicted with prostate can
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                                                                                                                           English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a patient; cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a patient
                                                                                (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) comprising of the
                                                                ) comprising of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Query Match
Best Local Similarity
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proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammacory activities, and can be us in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therap; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                         New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC98823 standard; cDNA; 1527
                                                                                                                                       AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                           Claim 1; Page 531-532; 1379pp; English.
                                                                                                                                                                                                                                                                                 WPI; 2000-579444/54.
P-PSDB; AAB54058.
                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
detection; diagnosis; identification; cytostatic; neuroprotect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC98823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G G

    is also useful as a pharmacodyanamic or

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monitoring the progression of prostate cancer in a patient; assessing the efficacy of a test compound to inhibit prosta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US05989
                                                                                                                                                                                                                                                                                                                                                                                                         99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer antigen nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:51.
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                                                                       and can be used
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RESULT 5
AAZ98108
ID AAZ9
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Best Local S
Matches 32
                                                                                                                                                                                                                                                           15-JUL-1998;
15-JUL-1998;
15-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; nootropic; neuroprofective; antiallergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; immune system disorder; arthritis; autoimmune disease; hepatic disease; renal disease; inflammation; Alzheimer's disease; behavioural disorder; schizophrenia; osteopporosis; antiportier; schizophrenia; osteopporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins can be identified. The pancreatic cancer antigens can be used detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; AIDS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis; acne; psoriasis; cardiovascular disorder; reproductive disorder; gastrointestinal disorder; respiratory disorder; metabolic disorder; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein encoding nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1527 BP; 397 A; 426 C; 394 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences
                                                                                                                                                           Lafleur DW,
Mucenski M,
                                                                                                                                                                                                                                                                                                                             14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ98108 standard; cDNA; 1722
                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                           27-JAN-2000
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                                                                                                                                                                                             MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention.
                                                                                                                                                          Komatsoulis G, Duan
, Ebner R, Olsen HS,
, Endress GA, Soppet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                           98US-0092921.
98US-0092922.
98US-0092956.
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100.0%; Pr
170 0;
                                                                                                                                                           Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32;
Pred. No.
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                                                                                                                                                             RD, KOSELL C...,
Brewer LA, Florence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Lc
o. 0.0043;
c. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 T; 2 other;
                                                                                                                                                                             Moore PA,
lorence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1527;
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                                                                                                                                                                           Shi Y;
Young
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The polynucleotide sequences given in AAZ98017 to AAZ98108

encode

the

New isolated human

neurological or blood

useful for diagnosis and

treatment

Page 370-371;

494pp;

English disorders 2000-161128/14. DB; AAY87155.

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CC human secreted proteins given in AAy87064 to AAY8723. Human secreted CC protein can have activities based on the tissues and cells the genes are CC expressed in. Examples of activities include: cytostatic; CC immunosuppressive; anttinflammatory; nootropic; neuroprotective; and CC antiallergic. The polynucleotides and their corresponding secreted CC polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions CC can be diagnosed by determining the amount of the new polypeptides in a CC sample or by determining the protein s and their polynucleotides can be used for developing products for the diagnosis or treatment of cancer, CC tumours, neurodegenerative disorders, developmental abnormalities and CC foetal deficiencies, blood disorders, developmental abnormalities and CC allergies, Alixheimer's disease, behavioural disorders, schizophrenia, CC allergies, Alixheimer's disease, behavioural disorders, schizophrenia, CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, CC transplant respections, diabetes, asthma, sepsis, acne, psoriasis, CC asidovascular disorders, reproductive disorders, gastrointestinal CC proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their of the proteins are also useful for identifying their first the proteins are food additives or proteins are food additives or proteins or polynucleotides of the protein of the protein are sequence used in the protein and protein and protein are sequence used in the protein and protein are sequence used in the protein are also useful for identifying their and the protein are also useful for identifying their and the protein are protein and anyering are sequence used in the protein are sequence used in the protein are protein and anyering are sequence used in the protein and protein anyering any protein and anyering anyering and anyering any protein any protein anyering anyering an
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system disorder; AIDS; autoimmune uisease; incumiental disorder; Barkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; inflammation; neurological disorder; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1722 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenic disorder; kidney disorder; gastrointestinal disorder;
pregnancy-related disorder; endocrine disorder; infection; wound
cell culture; chemotaxis; vulnerary; binding partner identificati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD11721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein-encoding gene 71 cDNA clone HDPOZ56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD11721 standard;
                           WO200151504-A1
                                                                                                                                                                                            sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abnormality; developmental abnormality; haematopoietic disorder; system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein; proliferative disorder; cancer; tumour; asthma;
abnormality; developmental abnormality; haematopoietic disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                     /*tag= b
122..1015
                                                                                                                                                                                                                                                                           /*tag= a
/product= "Human secreted
/transl_except= (pos:260...
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                               /product=
                                                                                                                                                                                               59..121
                                                                                                                                                                                                                    /transl_except=
/transl_except=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.3%;
                                                                                  "Mature
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Pred. No.
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                                                                                                                                                                                                                    n secreted protein precursor" (pos:260..262, aa:Xaa) (pos:401..403, aa:Xaa) (pos:695..697, aa:Xaa)
                                                                               human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 T; 5 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partner identification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergy;
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A AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted correction genes, and AAE060132 represent the proteins they encode. AAE06133-AAE06205 represent human secreted proteins fragments.

AAE06133-AAE06205 represent human secreted protein fragments.

AAE06133-AAE06205 represent human secreted protein fragments.

AAE06133-AAE06205 represent human secreted protein fragments.

CC AAE06133-AAE06205 represent human secreted protein fragments.

CC Pathological conditions and their genes are useful for preventing, treating correction in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 71 genes, correctly in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 71 genes, correctly disorders, for the diagnosis or treatment of proliferative correctly for the diagnosis or treatment of proliferative correctly for the diagnosis or treatment of proliferative consisting the protein and force of diseases (e.g., rheumaroid arthritis), inflammation, Allergies, conjuders (e.g., rheumaroid arthritis), inflammation, allergies, conjuders, epsis, diabetes, atherosolerosis, cardiovascular disorders, conjuders, endocrine disorders, skinney disorders, gastrointestinal disorders, correctly expressed, proteins can also be used to ald wound healing and epithelial cell correctly correctly of the invention can be used to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding correction of the invention can be used an alleviating symptoms associated correction of the invention can be used an alleviating symptoms associated correction of the invention can be used in alleviating symptoms associated correction of the invention can be used in alleviating symptoms associated correctly expressive or correctly expressive described protein encoding cDNA of the force of the protein of the correctly ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 737-738; 864pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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                                          present sequence represents a human secreted protein-encoding cDNA of invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muscenski M, Ebner R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brewer LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Rosen CA,
Florence KA,
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Young PE,
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Soppet DR;
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Sequence 1722 BP; 376 A; 534 C; 538 G; 269 T; Ç other;

QΥ Matches Query Match 1324 ТТТТСССБАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1354 Local Similarity Conservative 100.0%; 2.38; 0; Score 31; Pred Mismatches . No. DB 22; . 0.01; 0 Length 1722; 0 Gaps

0

ABK69818 RESULT ABK69818 standard; cDNA; 1722 BP.

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1655

TTTTCGGAAAAAAAAAAAAAAAAAAAAAAA 1685

Human secreted protein gene 71 #2

15-JUL-2002

(first entry)

ZZZZZZZZZZ ZZZZZZZZZZ Z ss; gene; secreted protein; gene therapy; immunosuppressive; tic; antirheumatic; antiproliferative; cytostatic; cardia cardiant;

Homo sapiens.

24-SEP-2001; 2001WO-US29871

04-APR-2002 WO200226931-A2

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CC The invention relates to an isolated nucleic acid molecule (or its C fragment, homologue complement or allelic variant) encoding a human CC secreted protein (and its fragment, domain, epitope, variant, secreted CC form and species variant). Also included are a recombinant vector CC comprising the nucleic acid, a recombinant host cell comprising the vector, an antibody against the secreted protein, a recombinant host cell comprising the cC vector, an antibody against the secreted protein, a recombinant host cell comprising the cC prevent, diagnose, treat or ameliorate a medical condition in e.g. CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep CC for example autoimmune diseases e.g. rheumatoid arthritis, cC hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, verebrovascular disorders e.g. cardiac arrest, verebrovascular disorders e.g. cardiac arrest, viruses and fungi and coular disorders are listed in the specification. Many other diseases and fungi and coular disorders are listed in the specification. The polypeptides can also be used as a food additive or prevent consumers. The polypeptides can also be used as a food additive or consument of the present consumers and of the invention. The present consumers and of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                  Novel 71 isolated secreted polypeptides and polypucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2000; 2000US-234925P.
12-JAN-2001; 2001WO-US00911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1219-1220; 1478pp; English
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, Olsen H, Brewer LA, Florence KA,
, Mucenski M, Ebner R;
                                                                                                                                                                         2.3%;
1843 BP
                                                                                                                                                                                                                                534 C; 538
                                                                                                                                                       Score 31; DB; Pred. No. 0.0
                                                                                                                                                         0;
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                                                                                                                                                                                                                            269 T; 5 other;
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Young PE,
                                                                                                                                                                                           Length 1722;
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Soppet DR;
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01-SEP-1998;
01-SEP-1998;
01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO1265 (UNQ636) cDNA sequence SEQ ID NO:83.
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18-SEP-1998;
                                 98US 0100662

98US 0100684

98US 0100684

98US 0100711

98US 0100919

98US 0100919

98US 01001044

98US 01010144

98US 0101071

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98US 0101071

98US 0101279

98US 0101472

98US 0101472

98US 0101473

98US 0101473
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98US-0100385.
98US-0100388.
98US-0100390.
98US-0100584.
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98US-0099642.
98US-0099741.
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RESULT 8 AAA37046 ID AAA3

AAA37046 standard; cDNA;

망 Q

Query Match Best Local Matches

Similarity

Conservative

Sequence 1722 BP;

376 A;

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30-SEP-1998;
30-SEP-1998;
30-SEP-1998;
30-SEP-1998;
01-OCT-1998;
02-OCT-1998;
07-OCT-1998;
07-OC
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29-SEP-1998;
30-SEP-1998;
GENENTECH
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9805-0103314

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9805-0103318

9805-0103328

9805-0103395

9805-0103401

9805-0103673

9805-0103673

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9805-0103711

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9805-0103711
                               9805-0105897

9805-0105887

9805-0105887

9805-0106023

9805-0106023

9805-0106033

9805-0106118

9805-0106118

9805-0106184

9805-0106584

9805-0106956

9805-0106956

9805-0106956

9805-0106956

9805-0106977

9805-0106978

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98US-0105104.
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INC
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Matches 31
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                                   Botstein
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Baker K,

Goddard A,

Gurney

ΑĽ,

Smith V,

Watanabe

CK,

Wood WI;

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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37130 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 49; 773pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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P-PSDB; AAY99364.
                                                                                                                                                                                                                  Sequence 1843 BP; 397 A; 564 C; 590 G; 292 T; 0 other;
                                                                                                      1 Similarity 100.
31; Conservative
                                                                                                                                 2.3%;
                                                                                                         0;
                                                                                                                                       Score 31;
Pred. No.
                                                                                                            Mismatches
                                                                                                                                       DB 21;
0.01;
                                                                                                                                                                  Length 1843;
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                                                                                                               0;
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AC AAXX
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29-APR-1998;
22-MAY-1998;
10-JUN-1998;
10-NOV-1998;
                                  WPI; 1999-430385/36.
P-PSDB; AAY06480.
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                                                                                                                               D, Goddard A, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; cDNA; 1844 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                        98US-0109304.
98US-0070440.
98US-0083500.
98US-0086414.
98US-0088742.
98US-0107783.
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79..141
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142..1779
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                                                                                                                                                                  Gurney AL,
                                                                                                                                                                  Hillan
                                                                                                                                                                  ĸJ,
                                                                                                                                                                  Lawrence DA;
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coding for human PRO1265 (UNQ036) (see AAVD6480). The clone was isolated from an adenoid tissue library. Amplification of DNA60764 on chromosome 19 occurs in various lung and colon tumours and cell lines, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed tot pRO1265 are expected to find use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX6477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1354
WPI; 2000-452188/39
P-PSDB; AAY93687.
                                                                                                                                                                                                                                                                                                                                                                             WO200037640-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding novel polypeptide PR01265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA46906 standard; cDNA; 1844 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1844 BP; 398 A; 564 C; 590 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 7; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody against proteins expressed tumor diagnosis and treatment
                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 31; Conserv
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                                                               Goddard
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                                                                                                                                 99WO-US28409.
99WO-US28301.
99WO-US28565.
                                                                                                                                                                                                      99WO-US20111
99WO-US21090
                                                                                                                                                                                                                                      99WO-US05028.
99WO-US12252.
                                                                                                                                                                                      99WO-US28313
                                                                                                                                                                                                                                                                                                          99WO-US30095
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 79..1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Sur
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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                                                               Gurney AL,
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Pred. No.
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                                                               Hillan
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0.01;
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                                                               Lawrence DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferation;
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                                                               Roy
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                                                               MA:
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Best Local S
Matches 31
                                             18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
                                                                                                                               06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                   20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343, PRO347, PRO315, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in mammals.
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                                                                                                                                                                                                                                                                                                                                      01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2000; 2000WO-US32678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS21481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 50; Fig 7; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation - \,
                                                                                                                                                                                                                                                     09-DEC-1999;
16-DEC-1999;
                                                                                                                                                                                                                                                                                         02-DEC-1999;
                                                                                                                                                                                                                                                                                                          02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence encoding for PR01265 polypeptide.
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31; Conserv
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2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
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                                                                                                                                                                                                                                                   99WO-US28565.
99US-0170262.
99WO-US30095.
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                                                                                                                                                                                                                                      99WO-US30911.
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100.0%; Pred. No. 0.
Live 0; Mismatches
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RESULT 10 AAA46906 ID AAA46

03-OCT-2000 AAA46906;

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1787

Query Match Best Local :

0

Matches

29-JUN-2000.

16-DEC-1999;

CDS

Homo sapiens

30-NOV-1999; 30-NOV-1999; 01-DEC-1999;

02-DEC-1999;

Botstein D, Wood WI;

08-MAR-1999; 02-JUN-1999; 01-SEP-1999;

15-SEP-1999;

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ARESULT 12
AADO2920
ID AADO2
XX AADO2
AC AADO2
XX 31-MA
XX 31-MA
XX Human
XX Human
KW antir
KW antir
KW antir
KW antid
KW antid
KW spanck
KW Spanck
KW Sarcc
KW demye
KW demye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC artilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by Sekeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC molecules involved in binding interactions. The polypucleotides encoding CC pRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.
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22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
10-NOV-2000;
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Smith V,
Human; PRO1265; antiinflammatory; dermatological; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antianaemic; haemostatic; antithyroid; antidiabetic; antivarial; antipsoriatic; antiallergic; antiasthmatic; inhibitor; therapy; systemic lupus crythematosis; spondyloarthropathy; systemic sclerosis; systemic vasculitis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; autoimmune thrombocytopenis; immune-mediated renal disease; hepatitis; demyelinating polyneuropathy; Guillian-Barre syndrome; Whipple's disease; hepatobiliary disease; primary biliary cirrhosis; sclerosing cholangitis;
                                                                                                                                                                                                                                                                                                                                                                                                                    1787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other
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P-PSDB; AAU12409.
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                                                                                                                                                                                                                                                                                                                  AAD02920 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1844 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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er PRO polypeptides, link bioactive molecules to cells expressing
polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Fig 475; 813pp; English.
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ME, Goddard
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; 2000WO-US14042.
; 2000WO-US14941.
; 2000WO-US15264.
; 2000WO-US30873.
                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                   (DNA60764-1533).
                                                                                                                                                                                                                                                                                                                    CDNA; 1844
                                                                                                                                                                                                                                      entry)
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A, Godowski PJ, Gurney i
Tumas D, Watanabe CK, W
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Pred. No.
                                                                                                                                                                                                                                                                                                                      ВP
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. 0.01;
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y AL, Sherwood S;
Wood WI, Zhang Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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16-DEC-1999;
18-FEB-2000;
01-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory bowel disease; gluten-sensitive enteropathy; skin disease; allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria; eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection; idiopathic pulmonary fibrosis; graft-versus-host-disease; ss.
                                                                                                                                                                                                                                                                                                                        31-AUG-1999;
01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                           Goddard
                                                                                                                                                                                                                                     Watanabe
                                                                                                                                                                                                                                                        (GETH
                                                                                                                                                                                                                 2001-226690/23.
DB; AAY72874.
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                                                                                                                                                                                                                                e CK,
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                                                                                                                                                                                                                                     Godowski
Wood WJ
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99WO-US20111

99WO-US2018

2000WO-US04342

2000WO-US04342

2000WO-US0439

2000WO-US13705

2000WO-US13705

2000WO-US14042

2000WO-US14941
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/product=
79..141
/*tag= b
142..1779
/*tag= c
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/product=
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                                                                                                                                                                                                                                           Gurney
                                                                                                                                                                                                                                                                                                                                                                                   "Mature human PRO1265 protein"
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                                                                                                                                                                                                                                            Tumas
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New PRO polypeptides for treating immune related and infiammatory diseases such as rheumatoid arthritis, systemic vasculitis, asthma. autoimmune hemolytic anemia, and diabetes mellitus

Claim 2; Fig 1; 118pp; English

The present sequence is a cDNA (DNA60764-1533 clone) encoding PR01265 CC protein. PRO protein, its agonist or antagonist or its antibody which cc are capable of enhancing or inhibiting the proliferation of "lymphocytes co or of increasing the infiltration of inflammatory cells into a tissue care useful in the diagnosis and treatment of immune-related diseases cc in mammals. The PRO protein is useful for treating systemic lupus crythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic carthritis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, cc inflammatory myopathy. Sjoyren's syndrome, systemic vasculitis, clabetes mellitus, immune-mediated renal cisease, ce thyroiditis, diabetes mellitus, immune-mediated renal cisease, co demyelinating disease of the central or peripheral nervous system, cc disease, infectious or autoimmune chronic active hepatitis primary co disease, infectious or autoimmune chronic active hepatitis, primary co disease, infectious or autoimmune chronic active hepatitis, primary co disease, autoimmune commune such as bullous cc sin disease, erythema multiforme and contact dermatitis, psoriasis, cc allergic diseases such as such as bullous such as eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyperconsitivity and urticaria, immunologic diseases such as bullous consitivity and urticaria, immunologic diseases such as bullous consistivity and urticaria, immunologic diseases of the lung consistiv

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Sequence 1844 BP;

398 A; 564 C;

590 G;

292 T; 0 other;

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1787

TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1817

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RESULT 13
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Best Local :
                                                     Query Match
                                  Matches
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26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
29-OCV-1999;
30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
                                                                               probes, in chromosoume unit may also be used used the sense RNA and DNA. They may also be used used in turn usef transgenic animals or knockout animals which are in turn usef development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                                                                                 Baker KP, Botstein
Gao W, Goddard A,
Pan J, Paoni NF, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1787 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1817
            1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                       The
                                                                                                                                                                                                                   therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200078961-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted; transmembrane; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding protein of the invention #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF54260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF54260 standard; DNA; 1844 BP.
                                                                              Sequence 1844 BP;
                                                                                                                                                          These proteins and the
                                                                                                                                                                                             Claim 2; Fig
                                                                                                                                                                                                                                          Secreted and
                                                                                                                                                                                                                                                                 WPI; 2001-071395/08
                                                                                                                                                                                                                                                                                        Watanabe
                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-2000; 2000WO-US04342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2000.
                                            Local
                                                                                                                                     present invention relates to secreted and transmembrane proteins see proteins and the DNA encoding them may be used as hybridization bes, in chromosome and gene mapping and in the generation of the sense RNA and DNA. They may also be used used to generate either
.ea and transmembrane
as hybridization pro
                                              Similarity
                                                                                                                                                                                                                                                                                        Paoni NF, Roy MA,
E CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                     99US-0162506
99WO-US28313
99WO-US28551
99WO-US30095
2000WO-US00219
2000WO-US00376
                                  Conservative
                                                                                                                                                                                            49; 787pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US20111
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9908-0145698
                                                                              398 A; 564 C;
                                                                                                                                                                                                                                                                                                            Godowski
                            2.3%; 5c.
100.0%; Pr
                                                                                                                                                                                                                             ane proteins probes, in c
                                                                                                                                                                                                                                                                                       Desnoyers L, Eaton DL, Ferrara N, owski PJ, Grimaldi CJ, Gurney AL, MA, Smith V, Stewart TA, Tumas D; PM, Wood WI;
                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                            Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31;
Pred. No.
                                                                              590 G;
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                                  Mismatches
                                                                                                                                                                                                                                 chromosome
                                               vo
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                                                                                                                                                                                                                             and nucleic acids designated PRO, chromosome and gene mapping and gene
                                                                              292 T; 0 other;
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. 0.01;
                                            DB 22
0.01;
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                                                       Length 1844;
                                  Indels
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                                                                                                                            useful for
                                                                                                                                                                                                                                                                                                              Fong S;
Hillan KJ;
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                                  Gaps
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The present sequence is one of twenty eight nucleic acids encoding PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, 'stromal and blastocoelic disorders, and inflammatory, anglogenic and immunological disorders.

to treat

Claim 20; Fig 23; 188pp; English.

Twenty eight nucleic acids encoding PRO polypeptides for treating various tumors, e.g. breast cancer, and inflammatory, angiogenic and immunological disorders

which other

are

useful

Baker KP, (Shelton DL,

Goddard A, ,, Smith V,

Gurney AL, Watanabe CK,

Hebert C, Wood WI;

Henzel

¥

Kabakoff RC;

P-PSDB;

2001-016509/02. DB; AAB50962.

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AAC91564
AC 91564
AC AAC
XX AA
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18-FEB-2000;
02-MAR-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general; antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant; PRO agonist; cancer; inflammatory disorder; immunological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC91564;
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11-FEB-2000;
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29-OCT-1999;
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2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
2000WO-US04342.
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99US-0141037.
99US-0144758.
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RESULT 15
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   Query Match
Best Local
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                           15-SEP-2000
18-SEP-2000
18-SEP-2000
24-OCT-2000
08-NOV-2000
08-NOV-2000
10-NOV-2000
20-DEC-2000
20-DEC
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25-JUL-2000
28-JUL-2000
02-AUG-2000
17-AUG-2000
23-AUG-2000
24-AUG-2000
27-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; angiogenesis; PRO protein; cardiovascularisation; wound atherosclerosis; cardiac hypertrophy; gene therapy; endothelia cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human anglogenesis related cDNA PRO1265 SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-2000;
(GETH
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                           2001US-0808689
2001US-0816744
2001US-0828366
2001US-0854208
2001US-0854208
2001US-0866028
2001US-0866034
2001US-0866034
2001US-0866034
2001US-0870574
2001US-0870574
2001US-0870574
2001US-0870574
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2001WO-US06520.
2001WO-US06666.
2001US-0802706.
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                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0665350.
2000US-242922P.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascularisation; wound; cancer;
phy; gene therapy; endothelial disorder;
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                           1787
                                                                                                                                                                                                                                                                                                                                                                                                                          1324 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAAA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or anglogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker KP,
Godowski k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GERB/)
(GERR/)
(GODD/)
(GODO/)
(GURN/)
(HILL/)
(MARS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 175; 567pp; English.
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(WATA/)
(WILL/)
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DB; ABB95510.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
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PAONI N F.
STEPHAN J F.
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GODDARD A.
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FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOOD W I.
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J, Gurney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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100.0%; Pr
0;
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ε CK,
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L, Hillan KJ, Marsters SA,
CK, Williams PM, Wood WI,
                                                                                                                                                                                                                                                                                                                                                               10:19:07
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Length 1844;

Indels

0;

Gaps

0

other;

Goddard SA, Pan J I, Ye W;

, T, Y,

Paoni NF;

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Title:

Sequence 43, Appl Sequence 21, Appl Sequence 31, Appl Sequence 30, Appl Sequence 30, Appl Sequence 20, Appl Sequence 25, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appli Sequence 5, Appli

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Minimum
Maximum
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-09-245-041-10
US-09-245-041-10
US-09-215-161A-10
US-09-215-161A-10
US-09-310-37A-6
US-09-340-993-1
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404.879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 385
LENGTH: 2943
TYPE: DUNA
ORGANISM: Homo sapiens
US-09-404-879A-385
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APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Hood, Thomas C.
APPLICANT: Otterness, Diane M.
APPLICANT: OTTERNESS, DIANE
APPLICANT: OTTERNESS, DI
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29, Application US/09167681A Patent No. 6265561
                                                                                 NUMBER OF SEQ ID NOS: 52
SOFTWARE: FRAKSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 7152
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Patent No. 6468546
                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/167,681A CURRENT FILING DATE: 1998-10-07 NUMBER OF SEQ ID NOS: 52
                             TYPE: DNA
ORGANISM: Homo sapiens
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US-08-819-867-57
US-09-91-097-21
US-09-924-838-3
US-08-527-678A-30
US-08-897-126-30
US-09-222-575-20
US-09-866-878A-25
US-09-387-212-2
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                       Sequence 1, Application US/09118256
Patent No. 6238864
GENERAL INFORMATION:
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Best Local
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CURRENT FILING DATE: 2001-02-08
TITLE OF INVENTION: ANALYTE DETECTION ASSAY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
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                PPLICANT: YAN, Lin
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
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NAME/KEY: CDS
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Pred. No.
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, OTHER INFORMATION: Description of Artificial Sequence: Adaptor 08\text{-}09\text{-}118\text{-}256\text{-}1
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LENGTH: 56
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SEQ ID NO 2
LENGTH: 56
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Best Local Similarity
Matches 27; Conserv
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SEQ ID NO 185
LENGTH: 558
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Patent No. 6331427
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CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,164
EARLIER FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 201.00010101
CURRENT APPLICATION NUMBER:
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CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,164
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                                                                                                                                                       APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-07-18
                                                                                                                   CURRENT FILING DATE: 1999-03-26 NUMBER OF SEQ ID NOS: 268
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                                                  TYPE: DNA
OTHER INFORMATION: ADAM family of
                                ORGANISM: Homo sapiens
                   FEATURE:
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; TYPE: DNA
; ORGANISM: human
US-09-265-630-4
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, NAME/KEY: misc_feature
, LOCATION: (1)..(558)
, OTHER INFORMATION: n = a,
US-09-280-116-185
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Best Local
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LENGTH: 654
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                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                           APPLICATION NUMBER: US/08/618,911 FILING DATE: Concurrently herewith ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                     APPLICANT: Hu, David
TITLE OF INVENTION: ALTERA
TITLE OF INVENTION: SEEDS
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
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ZIP: 50309
REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER:
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Hastings, Craig
Coughlan, Sean
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Best Local :
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
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                                                                                             FEATURE:
                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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Local Similarity 100.0%;
res 27; Conservative C
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                   LOCATION:
                                                                                NAME/KEY:
                                                                                                                       TOPOLOGY:
                                                                                                                                  STRANDEDNESS: single
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Hastings, Craig
Coughlan, Sean
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             DB 2;
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Best Local Similarity 100 Matches 27; Conservative

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RESULT 12
US-07-991-587A-6
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US-09-716-161A-10
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Best Local Similarity
Matches 27; Conserv
Sequence 6, Application US/07991587A Patent No. 5384249
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Best Local
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LENGTH: 1112
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                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/716,161A CURRENT FILING DATE: 2000-11-07
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVERTION: ANTISENSE MODULATION OF INTEGRIN BETA 4 BINDING PROTEIN EXPRESSIC
FILE REFERENCE: RTS-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 60/104,978
EARLIER FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: OF BODY WEIGHT DISORDERS FILE REFERENCE: 7853-136
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 131
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Nagle, D.
                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (71)...(808)
                                                                                                               1328 CGGAAAAAAAAAAAAAAAAAAAAAAA 1354
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Local Similarity 100.0%;
nes 27; Conservative (
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Pred. No.
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Pred. No.
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US-08-309-985-6
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Best Local
                                                                                                                                GENERAL INFORMATION:
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,758-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP-333661/1991
APPLICATION NUMBER: JP-091044/1992
FILING DATE: 17-12-1991
FILING DATE: 10-04-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM: Dos
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
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                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                  APPLICANT:
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                                                                                 APPLICANT:
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   NUMBER OF SEQUENCES:
                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELLETAX: LICENTELEFAX: 236262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                   PPLICANT:
                                                                                                                                                                                                                                                                                                       Local Similarity nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UPFILING DATE: 19930526 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence S. Perry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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277 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hasegawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212-758-2982
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      Hasegawa, Mamoru
/ENTION: '2 3 Sialyltransferase
EQUENCES: 7
                                                  Sekine, Susumu
Hanai, No. 5494790uo
                                                                                  Nishi, Tatsunari
                                                                                                Watanabe,
                                                                                                               Sasaki, Katsutoshi
                                                                                                                                                                                                                                                                                                         Conservative
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WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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No. 5384249uo
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Pred. No.
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. 0.023;
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Gaps

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APPLICANT: Tyrell E. NO. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM. 70296
CURRENT APPLICATION NUMBER: US/09/211/930
CURRENT FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-211-930-12
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 27; Conservative 0; Mismatches
                  SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 12 LENGTH: 2028
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Patent No. 5962265
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NFORMATION FOR SEQ ID NO:
TYPE: DNA
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OPERATING SYSTEM: Dos 3.3
SOFTWARE: WordDerfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-12-1991
FILING DATE: 10-04-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence S. Perry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELLING COLORION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/991,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
STREET: 277 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
CELL LINE:
CELL TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/991,587
FILING DATE: 16-12-1992
APPLICATION NUMBER: JP-333661/1991
APPLICATION NUMBER: JP-091044/1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 20-SEE
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melanoma
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В
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US-09-340-993-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вр
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US-09-211-930-12
Search completed: May 3, 2003, 11:28:51 Job time: 72 secs
                                                                                                                                 Query Match
Best Local Similarity
Matches 27; Conserva
                                                                                                                                                                                                                                                      SEQ ID NO 12
LENGTH: 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.0%;
Best Local Similarity 100.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Apparent No. 6034
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tyrell E. No. 6034228ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70296.N1
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930 EARLIER FILING DATE: 1997-12-19 & 1998-12-15
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                                                                                                  1328 CGGAAAAAAAAAAAAAAAAAAAAAAA 1354
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                                                                  1975 CGGAAAAAAAAAAAAAAAAAAAAAAAAAA 2001
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                                                                                                                                    Conservative
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Pred. No.
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n. 0.023;
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Title:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq
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Match
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length: 2000000000
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:/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB_Seq:*
:/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB_Seq:*
:/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB_Seq:*
:/cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB_Seq:*
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          2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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            0 US-09-925-297-51

US-09-984-271-102

US-10-001-054-23

US-10-053-107-1

US-10-028-072-475

US-10-123-904-475

US-10-123-904-475

US-10-140-470-475

US-10-176-918-475

US-10-176-921-475

US-10-176-921-475

US-10-140-474-475

US-10-142-431-475

US-10-143-114-475

US-10-143-114-475
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                       Sequence 102, Assequence 2, Apg Sequence 1, Apg Sequence 475, Assequence 475, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
>e.51, Appl 23, Appl 123, Appl 1 23, Appl 1 2475, Appl 24755, Appl 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 1527
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US-09-984-271-102
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US-09-925-297-51
  Sequence 102, Application US/09984271
Publication No. US20030040088A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
CURRENT FILING DATE: 7001-10-29
CURRENT FILING DATE: 7001-10-29
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Best Local
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA105
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US-10-124-819-475

US-10-124-822-475

US-10-124-822-475

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US-10-143-032-475
US-10-123-108-475
US-10-123-236-475
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC ITLE OF INVENTION: CELL GROWTH
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FILING DATE: 1998-03-27
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FILING DATE: 1998-07-15
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APPLICATION NUMBER: PCT/US99/15849
                                                       APPLICATION NUMBER: 60/085149
FILING DATE: 1998-05-12
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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FILING
             APPLICATION NUMBER: 60/090691
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FILING DATE: 2001-05-23
APPLICATION NUMBER: PCT/US01/17800
TT.TNG DATE: 2001-06-07
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FILING DATE: 2000-12-01
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APPLICATION NUMBER: PCT/US00/22031
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FILING DATE: 2001-02-28
APPLICATION NUMBER: PCT/US01/06666
FILING DATE: 2001-03-01
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APPLICATION NUMBER: PCT/US00/03565
FILING DATE: 2000-02-11
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SEQ ID NO 23
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PRIOR APPLICATION NUMBER: 60/107783
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APPLICATION NUMBER: PCT/US01/27099
FILING DATE: 2001-08-29
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No. US20020192752A1
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Hillan, Kenneth J
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NUMBER: PCT/US00/1494:
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SEQ ID NO 1
         PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
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                                                                                                                                 PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
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CURRENT FILING DATE: 2001-12-19
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APPLICATION NUMBER: PCT/US01/17800
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Watanabe, Colin K
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o. US20030004311A1
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NUMBER: 60/059263
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2.7e-06;
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APPLICATION NUMBER:
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; Sequence 475, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
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CURRENT FILING DATE: 2002-04-12
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PRIOR APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/091982
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Wood, William
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60/084600 60/083545 60/083322 APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082999

APPLICATION NUMBER:

FILING DATE: 1998-04-24

APPLICATION NUMBER: 60/081695

FILING DATE: 1998-04-

APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081203

FILING DATE:

1998-03-3

FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080165 APPLICATION NUMBER: 60/079728

APPLICATION NUMBER: 60/079663 FILING DATE: 1998-02-27

FILING DATE: 1998-03-25

FILING DATE: 1998-03-12 APPLICATION NUMBER: 60/0

1998-03-20

60/079294

60/078910

APPLICATION NUMBER: 60/085149 FILING DATE: 1998-05-12

FILING DATE: APPLICATION NUMBER:

1998-05-13

60/085338 60/085323

APPLICATION NUMBER: 60/

1998-06-19

60/089947 60/089907

APPLICATION NUMBER: FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599

FILING DATE: 19/98-06-11 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17

APPLICATION NUMBER:

FILING DATE: APPLICATION NUMBER: FILING DATE:

1998-06-10

60/088858

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APPLICATION NUMBER: FILING DATE: 1998-0

1998-06-04

60/088730

60/088026

60/087106 60/086430

FILING DATE: 1998-05-APPLICATION NUMBER: FILING DATE: 1998-05-22 APPLICATION NUMBER: FILING DATE: 1998-05APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-15 FILING DATE: 1998-05-15 APPLICATION NUMBER: FILING DATE:

APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15

APPLICATION NUMBER:

60/086414

APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 APPLICATION NUMBER:

1998-05-13

60/085579

FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/ APPLICATION NUMBER:

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US-10-140-470-475
US-10-140-475, Application US/10140470
; Sequence 475, Application US/10140470
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-475
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LENGTH: 1844
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                                                SEQ ID NO 475
LENGTH: 1844
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CURRENT FILING DATE: 2002-04-16
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NUMBER OF SEQ ID NOS: 550
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                                                                                                                                              TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C160
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                                                                             Prior Application removed - NUMBER OF SEQ ID NOS: 550
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Filvaroff, Ellen
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Watanabe, Colin K
Wood, William
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Gurney,Austin L.
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                                                                                                   See Palm or File Wrapper
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RESULT 10
US-10-176-918-475
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; Publication No.
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; ORGANISM: Homo Sapien
US-10-175-746-475
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US-10-175-746-475
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
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Best Local Similarity
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
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CURRENT FILING DATE: 2002-06-19
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Wood, William
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Filvaroff, Ellen
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                                                                                 Gerritsen, Mary E. Goddard, Audrey
                                                        Godowski, Paul J. Gurney, Austin L.
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Filvaroff, Ellen
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D. US20030027270A1
 Tumas, Daniel
             Stewart, Timothy A.
                            Smith, Victoria
                                           Sherwood, Steven
                                                                                                                Gao, Wei-Qiang
                                                                                                                                                           DeForge, Laura
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Pred. No.
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RESULT 11
US-10-176-921-475
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RESULT 12
US-10-137-865-475
: Sequence 475, Application US/10137865
: Publication No. US20030032155A1
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SEQ ID NO 475
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Best Local :
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CURRENT FILING DATE: 2002-06-20
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                                                                                                     1787 TTTTCGGAAAAAAAAAAAAAAAAAAAAAAA 1817
                                                                                                                                    1324 ТТТТСССАААЛААЛАЛАЛАЛАЛАЛАЛАЛАЛА 1354
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Wood,William
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Gurney, Austin L.
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Filvaroff, Ellen
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5. US20030027276A1
                                                                                                                                                                      Conservative
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                                                                                                                                                                                     Score 31;
Pred. No.
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o. 2.7e-06;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
TYPE: DNA
                          Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 475, Application US/10140474 Publication No. US20030032156A1
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Best Local Similarity 100.0%;
Matches 31; Conservative (
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                                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333ORIC162
                                                                                                    CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
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CURRENT FILING DATE: 2002-05-03
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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ORGANISM: Homo Sapien
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Gerritsen, Mary E.
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Wood,William
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Gurney, Austin L.
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Gurney, Austin L.
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Filvaroff, Ellen
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Pred. No.
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US-10-140-474-475

Query Match
Best Local Similarity
Matches 31; Conserv

2.3%; Score 31; DB 9; L dlarity 100.0%; Pred. No. 2.7e-06; Conservative 0; Mismatches 0;

Length 1844;

Indels

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Gaps

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; Prior Application removed - Se; NUMBER OF SEQ ID NOS: 550; SEQ ID NO 475; SEQ ID NO 475; LENGTH: 1844; TYPE: DNA; ORGANISM: Homo Saplen
US-10-142-431-475
                                                                                                                                                                                                                                                                                           RESULT 15
US-10-143-114-475
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US-10-142-431-475
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Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 31; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                              Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/142,431 CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                          Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                              Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                                                                   Beresini, Maureen
DeForge, Laura
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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                                                         Sherwood, Steven
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b. US20030036179A1
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                                                                                                                Query Match
Best Local Similarity 100.
Matches 31; Conservative
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 475
LENGTH: 1844
TYPE: DNA
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APPLICANT:
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CURRENT FILING DATE: 2002-05-09
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ACIDS FILE REFERENCE: P3330R1C211
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Wood, William
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SUMMARIES

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TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	CCU12314	RESULT 1
Investigation of peroxidase genes and genetic transformation in	ROSS, A.H.	1 (bases 1 to 1335)	clade; Panicoideae; Paniceae; Cenchrus,	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Cenchrus ciliaris	Cenchrus ciliaris.	•	U12314.1 GI:520567	U12314	Cenchrus ciliaris clone PX7 peroxidase mRNA, complete cds.	CCU12314 1335 bp mRNA linear PLN 02-AUG-1994		

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SLGTILSLEGGRUSARDMIALSGAHHAQARCTTFRGRIYGDTNIDASFAALQQOTCPR
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Oryza sativa (japonica cultivar-group) chi
OSJNBAO082C09, *** SEQUENCING IN PROGRESS
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 NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them
                                      Agrobiological Sciences, Rice Genome Research Program; Kannondal 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                              Sasaki,T., Matsumoto,T. and Katayose,Y. pirect Submission
                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DN clone:OSJNBa0082C09
                                                                                                                                                                                                                                                                                   Oryza satīva (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBa0082C09.
                                                                                                  Submitted (01-AUG-2002) Takuji Sasaki, National Institute
                                                                                                                                                         Published Only
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                                                                   CACCACCTTCCGCGGCCGCATCTACGGCGACACCGACATCAACGCCTCCTTCGCGGGCGCT
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
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Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrharroideae; Oryzeae; Oryza.
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laire,E., Young,S.A., Willard,L.H., McGee,J.D.,
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  RTSGDMNLAPLDTTANAFDNAYYNLLSNKGLLHSDQYLFNNGSTDNTVRNFASNAA
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                                                                                                                  ACGGTGAGGAACTTCGCGTCCAACGCGGCGGCGTTCAGCAGCGCCTTCGCGACGGCCATG
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RESULT 4 AF155124

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Gossypium hirsutum.
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 1369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF155124 1369 bp mRNA linear £LN 23-SEP-Gossypium hirsutum bacterial-induced peroxidase mRNA, complete AF155124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assighetse, K., Cuny.G., Valette, C., Delannoy, E., Bresson, E., Jalloul, A., Daniel, J.-F., Geiger, J.-P. and Nicole, M. Cloning and Characterization of a Bacterial-Induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jalloul, A., Bresson, E., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Physiol. 121 (1),
2 (bases 1 to 1369)
Assigbetse, K., Cuny, G.,
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/protein_id="AAD43561.1"
/protein_id="AAD43561.1"
/db_xref="GI:5453379"
/translation="MASTIPIVTLLIVMLSCHAANAQLSPNFY\aSCPNLQTIVRNAM
/translation="MASTIPIVTLLIVMLSCHAANAQLSPNFY\aSCPNLQTIVRNAM
SRAVNRETRIGASILALFEHDCFVNGCDGSILLDDTAAFTGTGEKAAVPNRNSARGFEVI
DTIKTNVEAACSATVSCADILALAARDGVALLGGFTMQVFLGRRDAFTASQSAANNQI
DTIKTNVEAACSATVSCADILALAARDGVALLGGFTTGLARCTTFRGRIYNDTNIDANFAAT
RRANCFAASGGDNNLAFLDIOTFTRFDNDYFRNLVARRGLLHSUQELFNGGSQDALVRT
RRANCFAASGGDNNLAFLDIOTFTRFDNDYFRNLVARRGLLHSUQELFNGGSQDALVRT
                                                                                                                                                                                                                         /note="proximal histidine; order(708. .710,783. .785)
                                                                                                                                                                                                                                                                                                            /note="distal histidine; av
order(312. .314,327. .329)
/note="disulfide bond"
order(471. .473,1050. .105
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1005. 1007
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                                                             /evidence=not_experimental 323 c 284 g 389
                                                                                                                                                                                                                                                                     /note="disulfide bond"
587. .689
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/dev_stage="2 week old
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/cultivar="Reba B50"
                                                                                                    1005. .1007
/note="glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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      Score 365.4;
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                                                                CCAACCAAAACTCTGTTAGAGGGTTCGACATAATAGACACGATCAAGACCAGAGTTGAGG
                                                                                                CGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAGG
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/protein_id="AAC05277.1"
/protein_id="AAC05277.1"
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TNLFTNKGLTARDVTLISGAHTIGGARTIFRORIYNDTNIDFAFATTRRGNCPQAGA
GANLAPLDGTPTQFDNRYYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAATFATD
FAAAMWRMGNISPLTGTNGEIRENCRRN"
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/dev_stage="21 day"
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/cultivar="Stormont Cirrus"
/db_xref="taxon:4006"
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/EC_number="1.11.1.7"
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Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Submitted (01-MUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7444], Fax:81-298-388-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them
                                                                                                                                                                                 Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA, clone:01077_A12
Published Only in Database (2001)
2 (bases 1 to 149417)
                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OJ1077_A12.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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ACCAGGAGCTGTTCGCCGCCGGCGGCGGCGGCAGGTCGTCGTCGCAGGACCCGCTGGTGC
                                      ACCAGGAGCTCTTCAACGGCGG----
                                                                                ACGTGTTCGACAACGGCTACTTCCGCGAGCTGACGAAGCAGCGCGGGCTGCTGCACTCGG
                                                                                                                                                               TGTGCCCCGCGGGCACCGGCGACGGCAACCTCGCGCCGCTGGACGCCGAGACGCCCG
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
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Oryza sativa
Oryza sativa
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Cryza sativa
Lukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varidiplantae; Streptophyta; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1287)
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Submitted (07-JUN-1992) C. Reimmann, Institute for Plant Biology,
University of Zuerich, Zollikerstrasse 107, CH-8008 Zuerich,
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/translation="masatnssis:kmllvaaamasvasaqlsatfydtscpnalstik
SvitaavnsearmgasllehehdcfvQgcdasvllsgqgeQnagpnvgslegeSyIdn
skarvealconfvgcadilavaardsvvalggpsmyvllgrdsftasalantdpa
akarvealconfvscadilavaardsvvalggpsmyvllgrdsftynetnidsafarqqq
pssslaelignfsrkgldatdmvalsgahtigqaqcqnfrdrivnetnidsafarqqqq
ancprptgsgdsnlapvdttpnafdnayysnllsnkgllhsdqvlfnggsadntvrn
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/EC_number="1.11.1.7"
377 c 353 g
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/protein_id="CAA46916.1"
/db_xref="GI:20286"
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/clone="pPIR3"
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              TGCCGGGTCGTCAACAGCTAGATACGACGCA 1018
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                                                                                                                    GCGCTGGTGAGGCAGTACAGCGCCAGCGCCTCGCTCTTCAACGCCGACTTCGTGGCAGCC
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RESULT 8
AF014467
LOCUS
DEFINITION
ACCESSION SOURCE KEYWORDS VERSION

REFERENCE AUTHORS Eukaryota; Viridiplantae; Streptophyta; Em Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzae; Oryza. 1 (bases 1 to 1306) Chittoor,J.M., Leach,J.E. and White,F.F. AF014467 1306 bp mRNA linear FOYZa sativa peroxidase (POX22.3) mRNA, complete cds. AF014467 Oryza sativa. Oryza sativa defense response gene; bacterial blight. AF014467.1 GI:2429285 Embryophyta; a; Poales, Po Poaceae; PLN Tracheophyta; 27-SEP-1997

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                    TCGCTCGCCAACAGCAACCCCCCGCCCCCGACGGCCAGCCTCGGCACGCTCATCTCCCTG
                                                                CTGGGAGGGCCATCATGGACGGTTCTGTTGGGGAGAAGGGACTCCACCACTGCAAGCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-JUL-1997) Plant Throckmorton Hall, Manhattan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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/strain="IRBB10"
/db_xref="taxon:4530"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FASNAAAFSSAFTTAMVKMGNISPLTGTQGQIRLSCSKVNS"
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/codon_start=1
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/tissue_type="leaf"
/note="mank isolated from rice
infiltration with incompatible
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Submitted (15-JUL-1994) Annette H. Ross,
Botany, St. Lucia, Brisbane, Queensland,
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Cenchrus ciliaris clone
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Spermatophyta; Magnoliophyta; Liliopsida;
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|cultivar="Biloela"
|/db_xref="taxon:35872"
|/tissue_type="wounded and unw/tissue_tib="lambda gt-10"
                 /product="peroxidase"
/protein_id="AAA20473.1"
/db_xref="GI:520570"
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    translation="MASSVSGLLLMLCMAAVASAQLSATFYDTSCPNALSTIKSAVTA"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; אייניים אייניים אייניים אייניים בייניים אייניים א
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Oryza sativa L. (strain Nipponbare, sub_species japonica) root cDNA to mRNA, clone R2576.
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Minobe, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (E-mail:MINOBE@rtcs0.riken.go.jp, Tel:0298-38-7441, Fax:0298-38-7468)
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Peroxidase from rice cDNA
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TOVEALCSQTYSCADILAYAARDSYVALGGESWTVLLGRRDSTAANESQANTDLFAPS
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                                  AP003544 135792 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 6 *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP003544.1 GI:13810550
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Published Only in Database (2001)
2 (bases 1 to 135792)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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NOTE: It currently consists of l contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                    Chittoor, J.M., Leach, J.E. and will birect Submission
Direct Submission
Submitted (18-JUL-1997) Plant Pathology, Kansas
Submitted (18-JUL-1997) Ranhattan, KS 66506, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chittoor, J.M., Leach, J.E. and White, F.F.
Differential induction of a peroxidase gene family during
of rice by Xanthomonas oryzae pv. oryzae
Mol. Plant Microbe Interact. 10 (7), 861-871 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa peroxidase
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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infiltration with incompatible strain of Xanthomonas
oryzae pv. oryzae"
                                                                                                                                                                                                                                                            /organism="Oryza sativa"
/strain="IRBB10"
/db_xref="taxon:4530"
/chromosome="7"
                                                                                                     /gene="POX8.1"
43. .990
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                               'gene="POX8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1220 bp mRNA linear (POX8.1) mRNA, complete cds.
                                                              inducible'
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Embryophyta; Tracheophyta; a; Poales; Poaceae;

infection

PLN

State University,

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BASE COUNT
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TCTCGTCGGCCATGGTGAAGATGGCCAACCTCGGACCACTCATCGGGAGCCAGGGACAGA
                          TCGTGGCAGCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGCCGGACAGA 976
                                                                            GGTCGCAGGACGCGCTGGTGAGGCAGTACAGCGCCAGCGCCTCCGCTCTTCAACGCCCAACT
                                                                                                                                       TCACCAACCTGTTCGCGGCGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCG
                                                                                                                                                                                                                   GCGACGGCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACT
                                                                                                                                                                                                                                                   ACATCGACGCCGGCTACGCGCGCGTCGCTCAGGGCCCAACTGCCCGCCGGCACGGCCACCG
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                                                            ACAGCACGACAACACGGTCAGGAACTTCGCCTCCAACAGGGCGGCGTTCAGCAGCGCCT
                                                                                                                        ACAGCAACCTGCTGTCCAACAAGGGGCTCCTGCACTCCGACCAGGTGCTCTTCAACGGCA
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92; Conservative
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FFDLENLIKAFGDKGFSYTDMVALSGAATIGOAQCTNFFGFIVNETNIDAGYAASLRA
NCPPTAGTGDSNLAALDTTTPYSFDTAYYSNLLSNKGLLHSDQVLFNGNSTDNTVRNF
ASNRAAFSSAFSSAMYKKANLGFLIGSQGQIRLSCSKVN"
a 368 c 330 g 237 t
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KEYWORDS
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                             156 GTCCTCCTGCCCAACCTGCAGAGCATCGTTCGGGCGGCGGCGATGACCCAGGCCGTCGCAAG
                                                                                                                                                                           96 GGTCGCCGTTTCCCTCCTCTGTGTCGCCCACGCACACGTTCTGCCCACGCTTCTATGC 155
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                                                                                                                                  GGTCGACGTTACGATAAGCTGTATACGAATTCCGGCGCAGTTGTCGCCGACGTTCTACGA 64
                                                                                                                                                                                                                                                                    al Similarity 61.6
559; Conservative
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HOrdeum vulgare partial mRNA for peroxidase (prx8 gene).
AJ276227
AJ276227.1 GI:9501335
peroxidase; prx8 gene.
Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 930)
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Green,R.M. and Bevan,M.
Isolation and characterisation
powdery mildew infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-JUL-2000) M. Bevan, 7UH, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan, M.
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/genr
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1 308 c 262 g
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43. .911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=3
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/franslation="EV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="prx8"
/function="defence against plant pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:112509"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="d8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare
/cultivar="Midas"
                                                                                                                                                                                                                                                                                                      25.0%;
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                                                                                                                                                                                                                                                                Score 339; DB 8;
Pred. No. 1.3e-39;
0; Mismatches 345
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Zea mays putative peroxidase
AF037034
AF037034.2 GI:15011985
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 1360)

Padegimas, L. S. and Reichert, N.A.

Isolation and characterization of peroxidase genes and regulatory
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On Jul 25, 2001 this sequence version replaced
Cocation/Qualifiers
1. .1360
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Padegimas, L.S. and R
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Padegimas, L.S. and Reichert, N.A.
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/protein_id="AAC79954.2"
/db_xref="GI:15011986"
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                                                                                              972 CCTCAGCCCCCAGACCGGAACCCAGGGGCAGATCAGGCGCAGCTGCTGGAAGGTCAACTC 1031
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Result
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                                                             345.6
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dopsis tl	AAC47449	21	1244		74.	40
radiata	AAA68189	21	646		75.	9
sativa p	AAH44071	22	1204		82.	8
radiata p	AAA68186	21	586	13.5	182.8	37
perenne	ABN87205	24	792		84.	86
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za sativa	AAH44090	22	1433		86.	ü
za sativa	AAH44091	22	1445		90.	2
sativa	AAH44078	22	1370		90.	31
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	AAH44086	22	1306		10.	29
sativa	AAH44076	22	1256		13.	28
sativa	AAH44075	22	1317		16.	27
sativa pe	AAH44074	22	1325		22	26
per5 ro	AAV63720	20	1355		26.	25
sativa	AAH44079	22	1137		31.	24
sativa p	AAH44084	22	1348			3
radiata	AAA68185	21	916		23	22
sativa	AAH44072	22	1218	17.4	236.2	21
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s radiata	AAA68192	21	801	•	268.6	12
sativa	4	22	N1		27	11
Pinus radiata pe	AAA68187	21	1224			10

ALIGNMENTS

RESULT 1 AAH44077 08-DEC-2000; 2000WO-JP08728 WO200142475-A1. CDS Oryza sativa Oryza sativa; rice; peroxidase; POX; characteristic; gene expression; modification; plant; bacterial infection; Magnaporthe grises; ss. Oryza sativa AAH44077 standard; cDNA; 1156 BP 14-JUN-2001. 12-SEP-2001 AAH44077; peroxidase s4235 encoding cDNA SEQ ID NO:13. (first entry) Location/Qualifiers 75..1058 /*tag= a /*tag= a /product= "peroxidase s4235"

Ohashi Y, Hiraga S;

Mitsuhara I,

Sasaki T,

Nagamura Y,

Ito Ħ,

īwai T;

(NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES

10-DEC-1999;

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Best Local Sim
Matches 650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AAH44071 to AAH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a peroxidase set by isolating RNA from the plant, binding the RNA to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New set of rice peroxidase genes for analysis of peroxidase exin rice under varying conditions and production of rice plants desired characteristics \,
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DB; AAB99738.
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                                                          CGCTCCTGTCGATGTTCAGCGCCAAGGGCCTCGACGCGCGGGACCTCACCGCGCTGTCGG
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                                                                                                   New set of rice peroxidase genes in rice under varying conditions desired characteristics -
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                                                            Page 183-186; 258pp; Japanese.
                                                                                                                                                                                                                                                                           Mitsuhara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rice; plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 53.1033 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "peroxidase s10927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peroxidase; POX; characteristic; g
; bacterial infection; Magnaporthe
                                                                                                                                                                                                                                                                           Η,
                                                                                                                                                                                                                                                                             Sasaki T,
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                                                                                                                                                                                                                                                                           Nagamura
                                                                                                                           analysis of production of
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                                                                                                                              f peroxidase
of rice plan
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                                                                                                                                                                                                                                                                                 Ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            grisea;
                                                                                                                                plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression;
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The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and

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Best Local Similarity 67.2%;
Matches 604; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragments, where the sequences of the peroxidase genes in the set are given in AAH44071 to AAH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1171 BP; 172 A; 429 C; 362 G; 208 T; 0 other;
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                                                                                                                   CGTTCGGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAAGGATGGGCCGCCTCTCTGCT 242
                CCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTGAGGCAGTACAG
                                                                       GACGCCGGTGAGGTTCGACACGGCCTACTTCACCAACCTGCTGTCGCGGCGGGGCCTGTT
                                                                                                                                                                                             CACCACCTTCCGCGGCCGCATCTACGGCGACACCCGACATCAACGCCTCCTTCGCGGCGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCGCGGGCGCAGCTGTCGCCGGGGGTTCTACTCGGCGAGCTGCCCCCACCGTGCACGGCGT 192
GCACTCCGACCAGGAGCTGTTCAACAACGGGCCGGTGGACTCGGTGGTGCAGCTGTACAG
                                                                                                                                                                               CGTCAACTTCCGCACCCGCGTCTACTGCGACGCCAACGTGAGCCCGGCGTTCGCGTCGCA
                                                                                                                                                                                                                                                                                                     CGACCTCCCGGGCCCGAGGCCGACATCTCCGCGCTCGTCTCCGCCTTCGCCGCCAAGGG
                                                                                                                                                                                                                                                                                                                                                                CTGGCCGGTGCCGCCGCCGCCGACGCGCTGTCGCCGAGTCGGAGCGCGGTGTCGAC
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                                                          Score 401; DB 22; Length 1171;
Pred. No. 5.9e-68;
0; Mismatches 280; Indels 15
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ARH44/BY
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AX AAH4
AX AAH4
AX AAH4
AX OAH4
AX OYZ
XX OYZ
XX WW MOOO
SS OYZ
XX KW MOOO
SS OYZ
XX KW MOOO
SS OYZ
XX MW MOOO
SS OYZ
XX WW20
PM W020
PM W020
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                                               The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AnH44071 to AnH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC in the sample plant; and (4) DNA microarrays for peroxidase gene CC expression analysis. The set of genes are used for the analysis of the CC pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC peroxidase gene expression to impart particular characteristics to the CC plants such as response to bacterial infection by Magnaporthe grisea.
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Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New set of rice peroxidase genes in rice under varying conditions desired characteristics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa; rice; peroxidase; POX; characteristic; gene expression; modification; plant; bacterial infection; Magnaporthe grisea; ss.
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P-PSDB; AAB99746.
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/product= "peroxidase
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Query Match Best Local S Matches 592

Similarity

26.6%; 63.1%; A; 401 C;

Score 360.8; Pred. No. 3.1e-60,); Mismatches 33

DB 22; T; 0 other;

Length 1310;

Gaps

2

Conservative

0;

1310

B₽;

297

354

G; 258

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RESULT 4
AAH44083
ID AAH4
XX
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XX
AC 12-9
  12-SEP-2001
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                       AAH44083;
                                             AAH44083
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                                                                                                              CCGCCGGACAGATCAGGCGCAACTGCCGGGTCGTCAAC 1002
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                                                                                                                                                                                                                                                        ACACGGCCTACTTCACCAACCTGCTGTCGCGGGGGGCCTGTTCCACTCGGACCAGGAGC
                                                                                                                                                                                                                                                                               CGACGGCAGCGGCGACACCTGGCGCCGCTGGACACGACGACGACGACGACGACGACGACGACGCCTTCG
                                                                                                                                                                                                                                                                                                    C-----CGGCGGCGACGCCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCG
                                                                                                                                                                                                                                                                                                                         ACAACGAGACAAACATCGACTCCAGCTTCGCGACGGCGCTCAAGGCCCAACTGCCCACGGC
                                                                                                                                                                                                                                                                                                                                     ACGGCGACACCGACATCAACGCCTCCTTCGCGGCGCTGCGCAGCAGACGTGCCCGCGGT
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                                                                                                   CCCAGGGGCAGATCAGGCTCAACTGCTCCAAGGTTAAC
                                                                                                                                              TCAACAGCGCCTTCACGGCGGCCATGGTGAAGATGGGGAACATCTCGCCCTTGACTGGAA
                                                                                                                                                                                          TCTTCAACGGCGGCAGCACGACAACACGGTCAGGAACTTCTCCTCCAACACGGCGGCGT
                                                                                                                                                                                                              TCTTCAACGGCGGTCGCAGGACGCGCTGGTGAGGCAGTACAGCGCCAGCGCCTCGCTCT
                                                                                                                                                                   TCAACGCCGACTTCGTGGCAGCCATGATTAGGATGGGCAACGTTGGGGGTGCTCACCGGCA
                                             standard;
  (first
                                              CDNA; 1223
  entry)
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Ohashi Y,
Hiraga S;
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                                                                                                                                                                                                                                                                    Oryza sativa.
                                                                                                                                                                                                                                                                                             Oryza sativa; rice; peroxidase; POX; characteristic; 9 modification; plant; bacterial infection; Magnaporthe
                                                                                                                     08-DEC-2000;
                                                                                                                                              14-JUN-2001
                                                                                                                                                                                                                                                                                                                                       Oryza
                                                                                          10-DEC-1999;
                                                                                                                                                                         WO200142475-A1
                                                               (NORQ ) JAPAN MIN AGRIC FORESTRY &
2001-381695/40
                                                                                                                                                                                                                                                                                                                                       sativa
                                      Mitsuhara
                                                                                                                       2000WO-JP08728
                                                                                                                                                                                                                                                                                                                                       peroxidase s14493 encoding cDNA
                                                                                           99JP-0352472
                                                                                                                                                                                                 /*tag= a
                                                                                                                                                                                                                             Location/Qualifiers 20..982
                                      ı,
                                        Sasaki T,
                                                                                                                                                                                                    "peroxidase s14493"
                                                                                                                                                                                                                                                                                                     POX; characteristic; gene expression;
infection; Magnaporthe grisea; ss.
                                                                   FISHERIES
                                         Nagamura
                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                           ۲,
                                           Ito
                                                                                                                                                                                                                                                                                                                                             NO:25
                                           Ħ,
                                           Iwai
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New set of rice peroxidase genes for analysis of peroxidase in rice under varying conditions and production of rice plan desired characteristics - $\footnote{`}$ plants expression

Claim 1; Page 189-192; 258pp; Japanese.

The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC detecting the label signal to show which gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC in the sample plant; and (4) DNA microarrays for peroxidase gene CC expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, CC cand modification of rice plants to provide desired specificities of CC peroxidase gene expression to impart particular characteristics to the CC plants such as response to bacterial infection by Magnaporthe grisea.

Sequence 1223 BP; 234 A; 397 C; 338 G; 254 T; 0 other;

ω ••

Query Match Best Local Matches 593; 133 CAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCG 302 193 95 Local Similarity -CCGGAGGGGAGAAGACCGCCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATC 360 GCCGTGAACGCGGCGGTGGCCAGGGAGCCCCGCATGGGCGCCTCCCTGCTCAGGCTCCAC TTCCGGGGGGAGCAGGGTGCGTTCCCTAATGTCAACTCGCTGAGGGGATTCGAGGTCATC TTCCACGACTGCTTCGTTCAAGGCTGCGACGGATCGATCCTTCTCGACG------Conservative 26.3%; 0; Score 356; DB 22; Pred. No. 2.6e-59; Mismatches Length 1223; Indels 21; Gaps 252 192 214 334 274 301

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RRESULT 5
ABN87249
ID ABN87249
AC ABN88
AC ABN80
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DT 30-J
XX
Loli
KW cell
KW cell
KW ceff
KW caff
KW cinn
KW F5H;
KW ryes
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PD 04-1
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                                                                                        Lolium perenne; perennial ryegrass; plant; cell wall; lignification; cellulase; enzyme; lignin biosynthesis; cellulose degradation; CCOAMT; caffeoyl-CoA 3-0-methyltransferase; cinnamyl alcohol dehydrogenase; CAD; caffeic acid 0-methyltransferase; OMT; cinnamate-4-hydroxylase; C4H; cinnamoyl-CoA reductase; CCR; peroxidase; PER; ferulate-5-hydroxylase; PER; CELL; phenylalanine ammonia lyase; PAL; 4-coumarate-COA ligase; 4CL; ryegrass; fescue species; molecular genetic marker; gene; ss.
                                                                                                                                                                                                                                                                                                          ABN87249
                              WO200226994-A1
                                                                                                                                                                                                               Lolium perenne peroxidase 1 cDNA sequence SEQ ID NO:176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGACCACCGACCTGGGTAACTTCGTCACTAGCTTCGCCGGGAAAGGGCTCAGCCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTAGCATTAAGATGCAACTCGAGGCATCTTGCAGGCAGACCGTCTCCTGCGCCGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCACCGGCACCGCCGGACAGTCAGGCGCAACTGCCGGGTCGTCAACAGCTAGATACGA 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGCCCGCTTCAACGCCGACTTCGCCGCCGCCATGGTGCGCATGGGCGCCATCAGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                 CGCATCGGATTCGATCGATATACT 1038
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                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                          cDNA; 1295
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Best Loc Matches Query Match

Local Similarity

25.5%;

Score 345.6; DB 2 Pred. No. 2.6e-57; 0; Mismatches 339

DB 24; Length 339;

Indels · 12;

Gaps

ų.

Conservative

145

124

GCCCACGCACACCTCCCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATC 183

GCCATGGCGTCTCCCACCTTGATGCAATGCCTGGTCGCCGTTTCCCTCCTCTCCTGTGTC 123

GCCATGGCATCTGCCTCTTGCATTTCTTTGGTGTTGCTGGTGGCCCTGGCAGCCACGGCG 144

85 64

184

Sequence 1295 BP;

295 A; 420 C; 337 G; 241 T; 2 other;

В Ωy В Qy В Qy Ъ Qγ B δÃ 밁 QΥ

364

ACCATCAAGCGGAACGTCGAGGCCGCGTGCCCGGCGTCGTGTCGTGCGCCGACATCCTC GGCAACGAGCAGAACGCCCCGGAACGCCGGTTCGCTGTTTGGCTTCGGCGTCATCGAC GGAGGGGAGAAGACCGCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGAC AGGCTGCACTTCCACGACTGCTTTGTTAATGGCTGTGACG---CGTCCGTTCTGCTGTCG

423

381

363 321 303 264 243 204

304

322

244

ATCAAGAGCGGCGTGGCAGCCGCCGTGAGTAGCAACCCCCGCATGGGCGCGTCGCTGCTC GCGTCGGCGCAGCTGTCGACGTTCTACGACACGTCGTGCCCCAGGGCCCTGGCCACC

205

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CC a molecular genetic marker. (I) can be used for modifying lightin cell controlled prepared to make the controlled plant to manipulate cell controlled problem and controlled plant to manipulate cell controlled problem and controlled plant to manipulate cell controlled problem and controlled plant species, as controlled problem to screen libraries from the desired plant. Short controlled problem are useful in amplification protocols controlled problem and controlled colds or its fragments encoding homologous genes from DNA or RNA. (I) or its fragments encoding homologous controlled problem and controlled colds or its fragments and the malecular controlled problem and in marker assisted selection, particularly in tregrass and fescues, and in forage and turf grass improvement, e.g. contagging QTLs for herbage quality traits, dry matter digestibility, controlled stress tolerance, disease resistance, insect pest resistance, plant stature, leaf and stem colour. The present sequence from the present controlled present controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid encoding lignification and cellulase enzymes their related enzymes useful for modifying lignin biosynthesis cellulose degradation in plants to manipulate plant cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding caffeoyl-CoA 3-O-methyltransferase (CCOAMT), cinnamyl alcohol dehydrogenase (CAD), caffeic acid O-methyltransferase (OMT), contains the contains and contains a contains a contains a contains a contains a contains and contains a contains and contains a contains and contains a contains and contai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 105; 436pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention
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RESULT 6
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AAA44
XX AAA44
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                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa peroxidase r3025 encoding cDNA SEQ ID NO:19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH44080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH44080 standard; cDNA;
  Ohashi Y,
                                                                                                                                           08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502
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                                              (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                                                                               10-DEC-1999;
                                                                                                                                                                                                                                      WO200142475-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCCGGTGCACCACCTTCCGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTTCAGCAGCGCCTTCGCCACGGCCATGGTCAAGATGGGCAACATCTCGCCGCTCACA
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  Mitsuhara
                                                                                                                                           2000WO-JP08728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 rice; plant;
                                                                                             99JP-0352472
                                                                                                                                                                                                                                                                                /product=
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 14..997
                                                                                                                                                                                                                                                                                                                                                                                                                                                      peroxidase; POX; characteristic; gene expression;
bacterial infection; Magnaporthe grisea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1158
    Sasaki T,
                                                                                                                                                                                                                                                                                       "peroxidase r3025"
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Matches 580;

Conservative

Local Similarity

25.0%; 61.9%;

Score 338.6; Pred. No. 5.6

DB 22; Length 1158;

pred. No. 5.6e-56;
0; Mismatches 339; Indels

18;

Gaps

2

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The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and circumstants, where the sequences of the peroxidase genes in the set are given in ARH44071 to ARH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a generating with a labelled peroxidase gene set, incubating, and cetecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 171-174; 258pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New set of rice peroxidase genes in rice under varying conditions desired characteristics -
Sequence 1158 BP; 255 A; 322 C; 327 G; 254 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for analysis of peroxidase expression and production of rice plants with
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108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCGG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCCGCCCTGGTCGTGATGGTGGTGGTGGTGCTCGCCGGTCGCGGGGGGCGCTCGTGGGCGC 107
                                                                                TTGGTCGGAGAGACTCGCGCACGGCGAGCCTCAGCGGCGCAAACAACAACATCCCGCCGC
                                                                                                                                             TCGGGCGGGGACTCGACGACGGCCAGCGCCTCGCTCGCCAACAGCAGCACCCCCCGCCCC
                                                                                                                                                                                          TCGCGCTTGCCGCGCGCGACCGAACCAACCTTCTCGGCGGGCCGACCTGGAGCGTGCCGC
                                                                                                                                                                                                                                                         ACACCATCAAGCGGAACGTCGAGGCCGCGTGCCCCGGCGTCGTGTCGTGCGCCGACATCC
                                                                                                                                                                                                                                                                                                                       TCACCGGCGAGAAGACGGCGAACCCCAACAACGGCTCCGTCAGAGGGTTTGAGGTGATCG
                                                                                                                                                                                                                                                                                                                                         CCGGAGGGGAGAAGACCGCCGGGCCCGAACCTGAACTCGGTGCGCGGCTTTGASGTCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTGTCGCCGAGCTTCTACTCGTACTCGTGCCCGGGAGTGTTCAACGCGGTGAAGCGGG 167
ACATGGTCGCCCTCTCCGGATCTCACACCATTGGGCAAGCACGATGCACAAACTTCAGAG
                ACATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCCGGTGCACCTTCCGCG
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Вþ δÃ В

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
 Query Match 24.7%;
Best Local Similarity 64.4%;
Matches 583; Conservative
                                                                               The present sequence represents the cDNA sequence of a peroxidase P7X gene. The P7X gene is isolated from maize inbred line Mp307. Peroxidases reduce hydrogen peroxide or molecular oxygen in the presence of an electron donor. Plant peroxidases are involved in pathogen defence responses. DNA constructs or transcription cassettes comprising peroxidase P7X gene and its promoter are useful for providing nematode resistance in plants.
                                                                                                                                                                                                 Claim 1; Fig 3; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF90234
                                                                                                                                                                                                                                       Novel gene encoding peroxidase P7X protein, and its promoter, useful for producing transgenic plants that are resistant against nematode
                                                                                                                                                                                                                                                                                    WPI; 2001-355920/37
                                                                                                                                                                                                                                                                                                              Padegimas LS,
                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                24-NOV-2000; 2000WO-US30159
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200138485-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a peroxidase P7X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2001
                                                        Sequence 1379
                                                                                                                                                                                                                                                                                                                                         (UMIS ) UNIV MISSISSIPPI STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 TGACGGGATCAAACGGGGAGATCAGGAAGAACTGCAG 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 768 CCGTGTTCGAGAACAACTACTACAAGAACCTCGTCGTCAAGAAGGGGCTCCTGCATTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCATATATACAACGAAACCAACATCGACAGTGGCTTTGCGATGAGGAGGCAATCAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCAGGAGCTCTTCAATGGCGGAGCCACTGATGCTCTTGTTCAGTCTTACATAAGTAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGCATCTACGGCGACACCGACATCAACGCCTCCTTCGCGGCGCGCCGCCAGCAGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGCACATTCTTTGCGGATTTTGTGACGGGCATGATCAAGATGGGGGGACATCACACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P7X gene; pathogen defence; nematode resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                              Reichert
                                                                                                                                                                                                                                                                                                                                                                     9905-0167229
                                                        322 A; 420 C; 370 G; 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA; 1379
                                                                                                                                                                                                                                                                                                              NA
; Score 334.6;
; Pred. No. 3.4e
0; Mismatches
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 3.4e-55;
ches 309;
                                                        <del>-3</del>
                           DB 22;
                                                        0 other;
                           Length
                              1379;
 13;
Gaps
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Hiraga S;
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in rice under varying conditions
desired characteristics -
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P-PSDB; AAB99742.
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06-OCT-1999; 20-APR-2000 WO200022099-A1

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                                                                                                                                                                                                                                                                               ; lignin; radiata;
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                                                                                                                                                                                                                                                                               lignin biosynthetic pathway; Eucalyptus grandis; Monterey pine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated polynucleotides and proteins cencoding and representing the enzymes cinnamate 4-hydroxylase (C4H).-CC commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (CCP), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-coA reductase (CCR), phenylalanine ammonia-lyase (pAL), 4-commarate:COA ligase (4CL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC caffeic acid methyl transferase, caffecyl COA methyl transferase, caffecyl COA methyl transferase, caffecyl COA methyl transferase, classe, peroxidase, cytochrome p450 LXXIA, diphenol oxidase, flavanol commerate COA ligase, cytochrome p450 LXXIA, diphenol oxidase, flavanol commosition are involved in the lignin biosynthetic pathway. The composition and the structure of a plant, especially eucalyptus and pine composition and for modifying the activity of an enzyme involved in lignin content, composition and structure. They can be used for designing probes can be useful for detecting similar DNA and RNA sequences in any cransfers, and for PCR amplification. The lignin content can be efficiently composition and the polynucleotides. AAAB10449 represent polynucleotides. AAAB7908 to AAAB6301 and AAB16341 to CC exemplification of the present invention.
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Best Local :
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14-JUL-1999;
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                                                                                                                                                                                                                                                                                                     Pinus radiata
                                                                                                                                                                                                                                                                                                                                   Plant; lignin;
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                                                                                                                                                                                                                                                                                                                        lignin biosynthetic pathway; Eucalyptus grandis; Monterey pine; ds.
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99US-0143811.
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The present invention describes isolated polynucleotides and protein encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), commentyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase

s and proteins kylase (C4H), L transferase

encoding and representing commarate 3-hydroxylase (

Claim 1; Page 187-188;

213pp; English.

Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and

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laccase, peroxidase, ferulate-5-hydroxylase (FHH), alpha-amylase, caffeld acid methyl transferase, caffeoyl coA methyl transferase, coumerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavanoid hydroxylase, and isoflavone reductase, which are involved in the lighin biosynthetic pathway. The polynucleotides can be used for modulating lighin content, lighin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lighin biosynthetic pathway, and for producing a plant having altered lighin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any crganism and for PCR amplification. The lighin content can be efficiently analided using the polynucleotides. AAA69201 and AAB6341 to AAB6449 represent polynucleotides. AAA6998 to AAA68201 and AAB6341 to Canabitation of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCCCGACGCCAGCCTCGGCACGCTCATCTCCCTGTTCGGCAGGCCAGGCCTGTCGC
                                                                                                                                                                                              AGACGTGCCCGCGGTCCGGCGGCGGCGACCTTGGCGCCCATCGACGTGCAGACGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCTCCCGCTTCCAGTCTGAGCACACTCATCTCATCTTTTCAAGCTCACGGTCTTTCTA
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                                                       TCACATTTGACAACAAGTATTACTCTAATCTTAAAATACAGAAAGGACTTCTCCACTCCG
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                                                                                                           TGAGGTTCGACACGGCCTACTTCACCAACCTGCTGTCGCGGCGGGGCCTGTTCCACTCGG
                                                                                                                                                                                                                                                                                 TCAGAACTCGGATCTACAACGAAACGAACATTAACGCTGCTTTCGCTACATCTGTAAAGG
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Pred. No. 1.2e
0; Mismatches
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                                               The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with desired characteristics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 220-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oryza
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                   The present invention describes isolated polynucleotides and proteins CC encoding and representing the enzymes cinnamate 4 -hydroxylase (C4H), CC commarate 3 -hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (CRR), phenylalanine ammonia-lyase (PAD), cinnamoyl-CoA reductase CC (CRR), phenylalanine ammonia-lyase (PAL), 4-commarate:COA ligase (4CL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase, CC commerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, CC which are involved in the lignin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC species, and for modifying the activity of an enzyme involved in lignin CC content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any cransism and for PCR amplification. The lignin content can be efficiently composition and the polynucleotides. AAA67908 to AAA68201 and AAB16341 to CC exemplification of the present invention.
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 464; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and structure
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                                                                                                                                                                                                                                             Sequence 801 BP; 195 A; 217 C; 195 G; 194 T; 0 other;
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14-JUL-1999;
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153
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                                                                                                                                    CCTGGTCGCCGTTTCCCTCTCTCTGTGTCGCCCACGCACAGCTCTCGCCCCACGTTCTA 152
                                                                                                                     CTTTATCGCCTTGTTGATGTGTTCGACCGTTGCGTACGCGCAGCTTAGCGCAACGTTTTA
                                                                           GENESIS RES & DEV CORP LTD. FLETCHER CHALLENGE FORESTS LTD.
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99US-0143811.
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                                                                                                                                                                                19.8%; Score 268.6; DB 21; Length 60.7%; Pred. No. 1.5e-42; tive 0; Mismatches 289; Indels
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                                     Bloksberg LN, Havukkala
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FLETCHER CHALLENGE FORESTS LTD.
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99US-0143811.
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Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially encalyptus and pine species having altered lignin content, composition and structure

Claim 1; Page 184; 213pp; English.

The present invention describes isolated polynucleotides and proteins composing and representing the enzymes cinnamate 4-hydroxylase (C4H), ccommarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (CGR), phenylalanine ammonia-lyse (PAL), cinnamoyl-coA reductase (CGR), phenylalanine ammonia-lyse (PAL), 4-commarate:CoA ligase (ACL), coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), ccinferol glucosyl transferase, caffeoyl coA methyl transferase, clavenoid hydroxylase, and isoflavone reductase, clavenoid hydroxylase, and isoflavone reductase, clavenoid hydroxylase, and isoflavone reductase, composition and the structure of a plant, especially eucalyptus and pine composition and for modifylng the activity of an enzyme involved in lighin content, composition and structure. They can be used for designing probes content, composition and structure in a plant having altered lighin content, composition and structure. They can be used for designing probes can deprimers useful for detecting similar DNA and RNA sequences in any cranism and for PCR amplification. The light content can be efficiently condified using the polynucleotides. AAA67908 to AAA68201 and ABB16341 to CC exemplification of the present invention sequences used in the

Sequence 1391 BP; 399 A; 321 C; 307 G; 364 T; 0 other;

ĎВ 21;

Length 1391;

망 Вþ В Вb DЬ Query Match Best Local S Matches 505 652 472 600 412 540 352 480 300 420 360 184 300 720 244 Match 19.1%; Local Similarity 56.7%; GTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGCTC ACCITCCGCGGCCGCATCTACGGCGACACCGACATCAACGCCTCCTTCCGCGGCGCTGCGG TCAGTCAAGAACATGGTGGCTCTTTCTGGTTCACATACCATTGGCCTAGCGAGATGCACT ACCGTGCCGCTCGGGCGGCGGGACTCGACGACGGCCAGCGCCTCGCCCAACAGCAAC GAAGTGATCGACCGCATCAAGGCTAGTCTGGAGAAGGAGTGCCCTGGAGTGGTT FCCTGT GAGGTCATCGACACCATCAAGCGGAACGTCGAGGCCGCGTGCCCCGGCGTCGTCGTGC CGGCTGCACTTCCATGACTGCTTCGTCAATGGGTGCGATGCGTCGATATTGTTGGATGAC GCCCGTTGTAAGCTCTCACCGAGTCATTATCAATCAACATGTCCGAAAGCATTGTCGATT TCGCCGCGCGACATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCCGGTGCACC ATACCTCCACCTACTTCTAATCTCAGTGCTCTCATAACCAGCTTCGCTGCTCAGGGTCTT ACCGTAAGCTTAGGGAGAAAGGATTCCATTACTGCTAGCAGGAGCCTTGCTAACACCTCC GCAGATATCGTTGCCCTGGCTGCTCGCGACTCAGTCGTTCATTTGGGAGGTCCTTCATGG 505; Conservative Pred. No. 1.3e
0; Mismatches Score 258.6; Pred. No. 1.3 .3e-40; les 374; Indels 12; Gaps 651 591 659 471 599 411 351 479 419 243 359 183 711 719 299 ۲.

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RESULT 14
AAF62772
ID AAF62
                           The present sequence is a synthetic Nicotiana sylvestris peroxidase gene which is optimised for expression in plants. The sequence may be introduced into plants to produce insect-resistant plants, preferably maize. It is useful for controlling insects such as ostrinia nubilalis, Heliothis zea and Spodoptera frugiperda. The transgenic seeds and plants can be used for the breeding of improved plant lines which, for example, increase the effectiveness of conventional methods such as harbicide or pesticide treatment or allow the conventional methods to be dispensed with. The peroxidase enzymes can be used in multiple insect control strategies, resulting in maximal efficiency with minimal impact on the
                                                                                                                                                                                                                                                                Novel anionic peroxidase genes isolated from Nicotiana tomentisiformis and anionic peroxidase protein encoded by the genes, useful for producing plants resistant to insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tobacco; Nicotiana sylvestris; peroxidase;
transgenic plant; insect-resistant plant; (
Heliothis zea; Spodoptera frugiperda; ds.
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16-NOV-1999;
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Ostrinia nubilalis;
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                                                                                                                                                                                                    CAACCTGCTGTCGCGGGGGGGGGGTTTCCACTCGGACCAGGAGCTCTT-----CAACGG
                                                                                                                                                                                                                                                                           CAACCTGGCGCCCATC---GACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACTTCAC
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GATCCGCACCGACTGCAAGCGCGTGAAC
                             GATCAGGCGCAACTGCCGGGTCGTCAAC 1002
                                                                                 CTTCGTGGCAGCCATGATTAGGATGGGCCAACGTTGGGGTGCTCACCGGCACCGCCGGACA
                                                                                                                                                      CGGGTCGCAGGACGCCTGGTGAGGCAGTACAGCGCCAGCGCCTCGCTCTTCAACGCCGA
                                                                                                                                                                                    CAACCTCCAGAGCAACCAGGGCCTGCTCCAGACCGACCAGGAGCTGTTCAGCACCAGCGG
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                                                                                                                         CAGCGCCACCATCGCCATCGTGAACCGCTACGCCGGCAGCCCAGACCCAGTTCTTCGACGA
                                                                                                                                                                                                                                                                                                            CGTGGACGCCACCTTCCTGCAGACCCTCCAGGGCCATCTGCCCCCAGGGCGGCAACAACGG
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Pred. No. 8.
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Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel anionic peroxidase genes isolated from Nicotiana tomentisiformis and anionic peroxidase protein encoded by the genes, useful for producing plants resistant to insects \dot{\,}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 975 BP; 202 A; 376 C; 263 G; 134 T; 0 other;
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16-NOV-1999;
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CCTGCTGGACACCGACGGCACCCAGACCGAGAAGGACGCTGCTCCCAACGTGGGCGCCG-
                                                                                                                                                         CCTTCTCGACGCCGGAGG------GGAGAAGACCGCCGGGCCGAACCTGAACTCGGT
                                                                                                                                                                                                              CGCCAAGATCATCCGCCTGCACTTCCACGACTGCTTCGTGAACGGCTGCGACGGCAGCAT
                                                                                                                                                                                                                                                            CGCCTCTCTGCTCAGGCTCTTCTTCCACGACTGCTTCGTTCAAGGCTGCGACGGATCGAT
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99US-0165683.
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pred. No. 5.1e-38;
0; Mismatches 345;
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Дb	Qy	Db	Qy	Db	Qy	Дb	Qy	DЪ	Qγ	Вb	Qy	Db	Qy	Вþ	Qy	Db	Qy	Фb	Qy	Db	Qy
942 CGAGATCCGCACCGAGCGCGTGAAC 972	972 ACAGATCAGGCGCAACTGCCGGGTCGTCAAC 1002	882 CGACTTCGTGAGCAGCATGATCAAGCTGGGCAACATCAGTCCCCTGACCGGCACCAACGG 941	912 CGACTTCGTGGCAGCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGGCGG 971	822 CGGCAGCGCCACCATCGTGAACCGCTACGCCGGCAGCCAGACCCAGTTCTTCGA 881	852 CGGCGGGTCGCAGGACGCCTGGTGGGGCAGTACAGCGCCCAGCGCCTCGCTCTTCAACGC 911	762 CACCAACCTCCAGAACAACCAAGGCCTGCTCCAGACCAGACCAGGAGCTGTTCAGCACCAG 821	798 CACCAACCTGCTGTCGCGGGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAA 851	702 CGGCAACACCTTCACCAACCTGGACATCAGCACCCCCAACGACTTCGACAACGACTACTT 761	741 CGGCAACCTGGCGCCCATCGACGTGCAGCGCGGTGAGGTTCGACACGGCCTACTT 797	642 CACCGTGGACGCCACCTTCCTCCAGACCCTGCAGGGCATCTGCCCCCAGGGCGCGAACAA 701	681 CGACATCAACGCCTCCTTCGCGGCGCCTGCGCAGCAGACGTGCCCGCGGTCCGGCGGA 740	582 CCGCTGCGGCACCTTCGAGCAGAGACTGTTCAACTTCAGCGGCAGCGGCAACCCCGACCC 641	642 CCGGTGCACCTTCC	522 CAAGGGCATGGACCTGACCTGGTGGCCCAGAGCGGCGCCCACACCTTCGGTCGAGC 581	582 GCAGGGCCTGTCGCCGCGCGCGACATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAGGC 641	462 CAACAGCGACATCCCCAGCCCCTTCGAGACCCCCCGTGATGACCCCCCTGTTCACCAA 521	522 CAACAGCAACCCCCCCCCCCCCACGCCCAGCCTCGGCACGCTCATCTCCCTGTTCGGCAG 581	402 CCCTAGCTGCAGGTGCTGTTCGGCCGCAAGAACAGCCTGACTGCCAACCGCAGCGAGGC 461	462 GCCGACCTGGAGCGTGCCGCTCGGCGGCGGCGGCGGCCAGCGCCAGCGCCTCGCTCG	342 GGTGAGCTGCGCGACATCCTGAGCCTCGCGAGCGAGATCGGCGTGGCCGTGGCCGAGGG 401	402 CGTGTCGTGGGGCGACATCCTCGCGCTTGCCGCGCGCGCG

Search completed: May 3, 2003, 08:16:26
Job time: 247 secs

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Result
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DB seq length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
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Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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ALIGNMENTS

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356 TCATCGACACCATCAAGCGGAACGTCGAGGCCCGCGTGCCCCGGGGTCGTGTGGTGGGCCG 415	302CGGAGGGGAGAAGACCGCCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGG 355	248 TCTTCTTCCACGACTGCTTCGTTCAAGGCTGCGACGGATCGATC	188 GGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGGTCAGGC 247	128 ACGCACAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTC 187	Query Match 21.2%; Score 287.2; DB 4; Length 1171; Best Local Similarity 59.7%; Pred. No. 2.4e-51; Matches 528; Conservative 0; Mismatches 338; Indels 18; Gaps	RESULT 1 US-09-615-192A-369 Sequence 369, Application US/09615192A Patent No. 6410718 GENERAL INFORMATION: APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1997-09-11 PRIOR APPLICATION NUMBER: US 09/169,789 PRIOR APPLICATION NUMBER: US 09/169,789 PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 369 LENGTH: 1171 TYPE: DNA ORGANISM: Pinus radiata

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CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
                                                                                                          ; TYPE: DNA
; ORGANISM: Pinus
US-09-615-192A-363
                                                                                                                                                  NUMBL.. Fast
SOFTWARE: Fast
SEQ ID NO 363
FRIGTH: 1224
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Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for
TITLE OF INVENTION: Modification of Plant Lign
                                     Query Match
Best Local Similarity 58.1
Matches 510; Conservative
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APPLICANT: HAVEKALA, TIKKA
TITLE OF INVENTION: Materials and Methods fo:
TITLE OF INVENTION: Modification of Plant Lig
FILE REFERENCE: 11000.1003c40
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
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                                                                                                                                          Sequence 368, Application US/09615192A Patent No. 6410718 GENERAL INFORMATION:
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Content.

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; PRIOR APPLICATION NUMBER: US 08/713,000; PRIOR FILING DATE: 1996-09-11; PRIOR APPLICATION NUMBER: US 09/169,789; PRIOR FILING DATE: 1998-10-09; NUMBER OF SEQ ID NOS: 405; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 368; LENGTH: 801; TYPE: DNA; ORGANISM: Pinus radiata
US-09-615-192A-368
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Best Local Similarity 60.7%;
Matches 464; Conservative
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                                                                                                                                                                                                                                                                                                           CAACCTGCTGTCGCGGCGGGGCCTGTTCCACTCGGACCAGGAGCT 845
                                                                   CGGCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACCGCCCTACTTCAC
                                                                                                                 CGACATCAACGCCTCCCTTCGCGGCGCGCTGCGGGAGCAGACGTGCCCGCGGTCCGGCGGCGAG
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AAATCTGAGAAGCCAAAAGGGACTTCTCCACTCCGACCAGCAGCT
                                                  CAACAACCTGTCACCATTGGATCGTGTTACTCCCACTACGTTTGACATCAACTACTACTC
                                                                                                     CAACATTAATGCAGCATACGCAACTTCCCTGAAGACAAACTGTCCGACTACAGGAAGCGA
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RESULT 4 US-09-615-192A-352 ; Sequence 352, Application US/09615192A ; Patent No. 6410718

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CORRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR ETLING DATE: 1997-11-21
PRIOR ETLING DATE: 1996-09-11
PRIOR PRIOR ETLING NUMBER: US 08/713,000
PRIOR ETLING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR ETLING DATE: 1988-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 352
LENGTH: 1391
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APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
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CCGACCTTCTTTGACAACCTTTACTACCACAATTTACTGCAGAAGAAGGGCCTTCTTCAC
                                 CCGGTGAGGTTCGACACGGCCTACTTCACCAACCTGCTGTCGCGGGGGGGCCTGTTCCAC
                                                                      CAGAAGATATGTCCCAGGATTGGAAATGATAGTGTCCTTCAAAGGCTAGACATCCAAACG
                                                                                                       CAGCAGACGTGCCGCGGTCCGGCGGCGACCGGCAACCTGGCGCCCATCGACGTGCAGACG
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APPLICANT: Lagrimini, Mark
APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6278041el Peroxidase Gene Sequences
FILE REFERENCE: S-31081pl
CUURRENT APPLICATION NUMBER: US/09/365,150
CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 975
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 58.3
Best Local Similarity 58.3
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                              465 CAGCGACATCCCCAGCCCCTTCGAGACCCTGGCCGTGATGATCCCCCCAGTTCACCAACAA
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                                                                                        TAGCTGGCAGGTGCTGTTCGGCCGCAAGGACAGCCTGACTGCCAACCGCCAGCGGCGCCCAA
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                                                         CGGCTTTGAGGTCATCGACCATCAAGCGGAACGTCGAGGCCGCGTGCCCCGGCGTCGT 404
                                                                                                                                                       GAGCTGCGCCGACATCCTGGCCCTCGCGAGCGAGATCGGCGTGGTGCTGGCCAAGGGCCC
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Pred. No. 1.6e-44;
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: tomentisiformis peroxidase gene

US-09-365-150-4
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US-09-365-150-4
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Patent No. 6278041
GENERAL INFORMATION:
APPLICANT: Lagrimini, Mark
APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6278041el Peroxidase
FILE REFERENCE: S-31881P1
                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
LENGTH: 975
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/365,150 CURRENT FILING DATE: 1999-07-30 NUMBER OF SEO ID NOS: 6 SOFTWARE: Patentin Ver. 2.0
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                                                                       CGCCTCTCTGCTCAGGCTCTTCCTTCCACGACTGCTTCCAAGGCTGCGACGGATCGAT
                                                                                                                     CCTGCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGG
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                 CTTCGTGAGCAGCATGATCAAGCTGGGCAACATCAGTCCCCTGACCGGCACCAACGGCCA
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CCTGCTGGACACCGACGCACCCAGACCGAGAAGGACGCTGCTCCCAACGTGGGCGCCG-
                                                                                                                                                                                                                                      544; Conservative
                                                        CGCCAAGATCATCCGCCTGCACTTCCACGACTGCTTCGTGAACGGCTGCGACGGCAGCAT
                                                                                                                                                                                                                                                  18.1%; Score 245; DB 4; Length 975 58.4%; Pred. No. 1.4e-42;
                                                                                                                                                                                                                                      Mismatches 345; Indels. 42;
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RESULT 7
US-09-615-192A-361
                                                                       CURRENT FILING DATE: 1907-10-28
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-10
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
             SOFTWARE: Fa
SEQ ID NO 361
LENGTH: 916
                                                                                                                                                                                                     Sequence 361, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, IIkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin C
FILE REFERENCE: 11000.1003c4U
                                                           NUMBER OF SEQ ID NOS:
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                                                                                                                                          Sequence 5, Patent No. 6
                                                                                         APPLICANT: Ainley
APPLICANT: Armstr
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, Application US/09097319A 6384207

Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F.

Armstrong, Ka Belmar, Scott Ainley, Michael

Katherine

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; ORGANISM: Pinus radiata US-09-615-192A-361
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Best Local Similarity
Matches 452; Conserv
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TCTTCAACGGAGGCTCCACTGATTCGCATGTGACTAAGTACGCCTCCAAC
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                 TCTTCAACGGCGGGTCGCAGGACGCGCGTGGTGAGGCAGTACAGCGCCAGC 894
                                                                                                                                       CCACAGGCTCCGGAGACAGCAACCTGTCGCCACTGGATTATACGACTCCCACTGTGTTTG
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                                                                  ACAAAAACTATTACTACAATCTGAAAAGCAAAAGAGGACTTCTCCACTCCGACCAGGAAC
                                                                                        ACACGGCCTACTTCACCAACCTGCTGTCGCGGGGGGCCTGTTCCACTCGGACCAGGAGC
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58.78;
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Pred. No. 2.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length. 916;
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Best Local :
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NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
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LENGTH: 1354 base pair
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Indianapolis
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/097,319A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DowElanco Patent Department
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                                                                         GGCGGGGGACTCGACGACGGCCAGCGCCTCGCCAACAGCAACCCCCCGCCCCGA 544
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                                                                                                               GCCGGAGAGACTCGCTCGGTGCAAGCATCCAGGGCTCCAACAATGACATCCCAGCCCCCA
                                                                                                                                                                         CCCTTGCGGCTCGTGATTCCACCGCCCTGGTTGGTGGACCATACTGGGACGTGCCACTTG
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TTGTCGCCCTCTCAGGTGGTCACACCATTGGTATGTCTCGGTGCACTAGTTTCCGGCAGA
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Pred. No. 1.1e-38;
0; Mismatches 359;
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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; LENGTH: 586
; TYPE: DNA
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                                                                                                                                                                                                                                                                           Query Match 13.5%; Score 182.8; DB 4; Best Local Similarity 61.2%; Pred. No. 1.2e-29; Matches 295; Conservative 0; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
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                                                             GCCCGGTGCACCACCTTCCGCGGCCGCATCTACGGCGACACCGACATCAA:GCCTCCTTC 699
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                                                                                                                    AGGCAGGGCCTGTCGCCGCGCGCACATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAG 639
  GCGGCGCTGCGGCAGCAGACGTGCCCGCGGCGCCGCCGACGGCAACCTGGCGCCCATC
                                          GCACGGTGCACCACATTCAGAACTCGCATCTACAACGATACCAACATTAACGCTGCCTTC 180
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; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-615-192A-365
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US-09-615-192A-365
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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Best Local Similarity
Matches 331; Conserv
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APPLICANT: Bloksberg,
APPLICANT: Havukkala,
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CCAACAACAATTCGTTGAGGGGTTTCGACGTCATAGACACCATCAAATCACAAGTGGAAG
                                        CGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAGG 385
                                                                                                                                                                                                                         GCGACGGATCGATCCTTCTCGACGCC-------GGAGGGGAGAAGACCGCCGGGC 325
                                                                                                                                                                                                                                                                                                  AGAAACGCATGGGGGCATCATTGCTCCGTCTTCACTTTCATGATTGTTTCGTCAAIGGTT
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Pred. No. 3.4e-28;
0; Mismatches 222;
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US-09-615-192A-359
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Best Local Similarity 54.6
Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 359, Application US/09615192A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE OF INVENIOR TO THE REFERENCE: 11000.103c4U CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 DRICH APPLICATION NUMBER: US 08/975,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
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                                                                                                                                                                                          276 CAGGGCTGTGATGCTTCAATTCTGCTTGATGACACTGCTAGTTTCACAGGGGGAGAAGACA 335
                                                                                                                                                                                                                                                                   216 AAAAAGGAAGCGAGAATGGCTGCTTCCTTGCTTCGTCTGCATTTTCATGACTGTTTTGTT
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                                                                                                              GCATTACCTAACAGAAATTCTGTAAGAGGCTTTGAGGTAGTGGATAAGATCAAAAGCAAA 395
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                                                                         GTCGAGGCCGCGTGCCCCGGCGTCGTGTCGTGCGCGCGACATCCTCGCGCGTTGCCGCGCGC 438
                                                                                                                                      GCCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAAC
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GENERAL INFORMATION:

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TITLE OF INVENTION: IO NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS

STREET: 10 S.
CITY: CHICAGO

ADDRESSEE

STATE: ILLINOIS COUNTRY: U.S.A.

60606

OPERATING SYSTEM:

CLASSIFICATION: APPLICATION NUMBER: FILING DATE: 28-FE -08-190-029A-9

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TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312-715-1000
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: JOHN J. MCDONNELL REGISTRATION NUMBER: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 9202401.7 FILING DATE: 05-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/
FILING DATE: 27-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 9116325.3
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o. 5736363
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10 S. WACKER DRIVE, SUITE 3000
                                                                                                                                                                   Homo sapiens
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                        /codon_start= 11
/function= "Gene for IGF-II/HRP fusion protein"
/product= "Synthetic DNA"
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; LOCATION: 857..1057
; OTHER INFORMATION: /fur
US-08-190-029A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 304
                                                                                                                                        Sequence 9, Applic Patent No. 5854025
GENERAL INFORMATION:
APPLICANT: BDWARDS, Richard Mark
APPLICANT: BAWDEN, Lindsey
TITLE OF INVENTION: IGF-II ANALOGUES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         494
                                                                                                                                                                                                                                                                                 554 ATGGATAGGCTCTACAATTTCAGCAACA 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 TTCCATGACTGCTTCGTGAATGGTTGCGACGCTAGCATATTACTGGACAACACCACCAGT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 TTCCGCACTGAAAAGGATGCATTCGGGAACGCTAACAGCGCCCAGGGGGCT"TCCAGTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GCCGGAGGGGAGAAGACCGCCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 TTCCACGACTGCTTCGTTCAAGGCTGCGACGGATCGATCCTTCTCGAC------- 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 CAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Sin
hes 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..6
OTHER INFORMATION: /function= "HindIII cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 ACAATCGTCAACGAGCTCAGATCCGATCCCAGGATCGCTGCTTCAATATTACGTCTGCAC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 CAGTTAACCCCTACATTCTACGACAATAGCTGTCCCAACGTGTCCAACATCGTTCGCGAC 73
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                                                                                                                                                                                                                                                                                                                      CGCGGCCGCATCTACGGCGACACCGACA 685
                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGACATGACGGCGCTGTCGGGCGCGCGCACACCATCGGGCAGGCCCGGTGCACCACCTTC
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                                                                                                                                                                                                                                                                                                                                                                       AGTGACCTTGTGGCTCTGTCCGGAGGACACACATTTGGAAAGAACCAGTGTAGGTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATTCTTCACCCTGCCCCAGCTGAAGGATAGCTTTAGAAACGTGGGTCTGAATCGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGACGGCCAGCCTCGGCACGCTCATCTCCCTGTTCGGCAGGCCAGGGCCTGTCGC---CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGACTATAGCTGCGCAACAGAGCGTGACTCTTGCAGGCGGACCGTCCTGGAGAGTGCCG
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                                                                                                                                                                 Application US/08462695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.8%;
53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function=
(fragment)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function= "IGF-II coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function= "EcoRI cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 119.6; DB
Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "HRP coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249;
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MOLECULE TYPE: ORIGINAL SOURCE:

ORGANISM:

NAME/KEY: CDS

11..1057

STRANDEDNESS:

nucleic acid

657

493 597

553

433 540 480

313

373

420

360

253

TOPOLOGY:

linear

OTHER INFORMATION: OTHER INFORMATION:

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                                                                                                                 US-08-462-695-9
                                      Query Match
Best Local Similarity
Matches 304; Conserv
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: LV _
CITY: CHICAGO
CTATE: ILLINOIS
TIS.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MCDONNELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9202401.7 FILING DATE: 05-FEB-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/01389

FILING DATE: 27-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 11..1057
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
133 CAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCG 192
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                                                                                                                             NAME/KEY: misc_feature LOCATION: 857..1057 OTHER INFORMATION: /fu
                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 11.856
OTHER INFORMATION: /fur
OTHER INFORMATION: (fra
                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 1067..1072 OTHER INFORMATION: /fur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 5-JUN CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /function= "HinDIII cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9116325.3 FILING DATE: 29-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 28-FEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BANNER & ALLEGRETTI, LTD.
STREET: 10 S. WACKER DRIVE, SUITE 3000
                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                      Conservative
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1..6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCDONNEL
                                                      53.5%;
                                                                                                                                                                                                     /function= "HRP coding sequence
(fragment)"
                                                                                                                                                                                                                                                                                              /function= "EcoRI cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start= 11
/function= "Gene for IGF-II/HRP fusion protein"
/product= "Synthetic DNA"
                                                                                                                           /function= "IGF-II coding sequence"
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                                                      Score 119.6; DB 2; Pred. No. 2e-16;
                                      Mismatches
                                    249;
                                    Indels
                                                                      Length 1072;
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                                  Gaps
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                                                                                                                                            US-09-615-192A-371
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                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                SOFTWARE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 371, Application US/09615192A Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                         Matches
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                   PRIOR EILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                          LENGTH: 1522
TYPE: DNA
ORGANISM: Pinus radiata
                                  136 CTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCGGCG 195
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182 CTTTCTTGGACGTTCTACAGCTCGAGTTGCCCGTCCTTGGAGTCCATAGTGTGGGAGCGC 241
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                                                                                      Match 8.8%;
Local Similarity 49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGGCCGCATCTACGGCGACACCGACA 685
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                                                                       443;
                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.0
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Havukkala, Ilkka
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TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Materials and Methods for the FILER OF INVENTION: Modification of Plant Lignin C FILER FERENCE: 11000.1003c4U CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR APPLICATION NUMBER: US 08/713,000
                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                        Sequence 370, Application US/09615192A Patent No. 6410718
                                                                                                                                        APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
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; PRIOR FILING DATE: 1996-09-11; PRIOR APPLICATION NUMBER: US 09/169,789; PRIOR APPLICATION NUMBER: US 09/169,789; NUMBER OF SEQ ID NOS: 405; SOFTWARE: FASTSEQ for Windows Version 3.; SEQ ID NO 370; LENGTH: 1073; TYPE: DNA 1073; ORGANISM: Pinus radiata
US-09-615-192A-370
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ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 1 AA979912 LOCUS COMMENT DEFINITION JOURNAL PCR PRIMETS
FORWARD: tw1412 (5'-GAAGATACCCCACCAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
BACKWARD: T0w: D column: 6
Plate: MEST3 row: D column: 6 Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings
Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. Plate: MEST3 row: D column: 6
Seq primer: tw1412 (5'-GAAGATACCCCACAAACC-3'). I lowa State University G405 Agronomy, Ames, IA 50011, Tel: (515)-294-0975 Fax: (515)-294-2299 AA979912.1 GI:3157290 EST. AA979912 848 bp mRNA linear EST 26-MAY-1998 MEST3-D6.TW1412.Seq ISUM2 Zea mays cDNA clone MEST3-D6.5', mRNA Email: schnable@iastate.edu Zea mays Zea mays. (bases 1 to 848) USA

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//dev_stage="""Wo-leaf-stage green seedling"
/lab_host="XLI-MFR Blue"
/lab_host="XLI
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/cultivar="B73"
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iowa State University G405 Agronomy, Iowa State University, Ames, Tel: 515-294-0975 Fax: 515-294-2299 Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14208180.
Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
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1 (bases 1 to 446)
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/clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
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/cultivar="B73"
/db_xref="taxon:4577"
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                                                                    677 ACACCGACATCAACGCCTCCTTCGCGGCGCTGCGGCAGCAGACGTGCCCGCGGTCCGGCG 736
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Zea mays
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On May 25, 2001 this sequence version replaced gi:14208633
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 538)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)...
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MEST29-D08.T3 ISUM4-TN Zea mays cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG842311.2
                                                                                                                                                                      Similarity
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/tissue_type="Seedling and silk"
/lab_host="DH10B"
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J.
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1 (bases 1 to 230)
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T18410.1 GI:474233
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                                                                                                              Seq primer:
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                                                                                                                                                  Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                              DNA Sequencing Core
University of Florida
                                                                                                                                                                                                                                                                                                                                                Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                     Chris Baysdorfer
Department of Biological Sciences, School of Science
California State University, Hayward
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ph: 602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
                                                                                                                                   E-mail: robferl@nervm.nerdc.ufl.edu
                                                                                                                                                                                                               P.O. Box 100695
                                                                                                                                                                                                                                                                                                                               E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                         Rob Ferl
                                                                                                                                                                                                                                                                      Interdisciplinary Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Plant Sciences, University of Arizona,
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/db_xref="taxon:4577"
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                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTAAGCAAGTAGCTTCATTCACCGAGCGTGCAGGCACAGGCAGCAGCAGCTTGCCATGGCG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCCCACCTTGATGCCAATGCCTGGTCGCCGCTTTCCCTCCTCTCTGTCGCCCCACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags
Unpublished (1997)
Contact: Schnable, PS.
Schnable laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                          FORWARD: T7-YJ (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
                                                                                                                                                                                                                                                                                                       PCR PRimers
FORWARD: tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wen, T.J., Ashlock, b.A. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings
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MEST3-D6.POLYT-N.Seg ISUM2 Ze
                                                                                                                                                                                                                                                                                                                                         Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 850)
                                                                                                                                                                                                                                                                                                                                                          State University
Agronomy, Ames, IA 50011,
(515)-294-0975
(515)-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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82 c 60 g 48 t 3 others
/tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
/note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECORI; Site_2: XhoI; ds-cDNA molecules were generated as
                                                                                                                        /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST3-D6"
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="etiolated seedling"
/lab_host="DH10B"
                                                                                                   /clone_lib="ISUM2"
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Pred. No.
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3-D6 5', mRNA
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DEFINITION
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62
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                               73 TCTCCCACCTTGATGCAATGCCTGG
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                                                                                GCTTAAGCAAGTAGCTTCATTCACCGAGCGTGCAGGCAGCAGCAGCAGCTTGCCATGGCG
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TCTCCCACCTTGATGCAATGCCTGG
                                                                 GCTTAAGCAAGTAGCTTCATTCACCGAGCGTGCAGGCACAGGCAGCAGCTTGCCATGGCG
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Zea mays
                                                                                                                                                                                                                                                                                                                                                Trait and Technology Development, Food and Feed Research Pioneer Hi-Bred International, Inc. 7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, Tel: 515 270 5934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM501068.1
EST.
                                                                                                                                                                                                                                                                                                                                     Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Jung R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM501068
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                                                                                                                                                                                                                                                                                                  rudolf.jung@pioneer.com
    .Location/Qualifiers
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                                                                                                                                                                                                                /db_xref="taxon:4577"
/clone_lib="Pioneer AF:1 array"
/note="Vector: pSport1; Site_1:
/note="Vector: pSport2" 77 t
                                                                                                                                                                                                                                                                                  /organism="Zea mays"
                                                                                                                                                  6.3%;
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Pred. No
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11 others
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ys cDNA,
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RESULT 8
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                         AGGCAGTACAGCGCCA 190
                                                                                                                                                                                                        BE597204 436 bp mRNA linear EST 18-AUG-2000 PI1_69_D10.gl_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA, mRNA sequence.
BE597204
                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC · clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 436)
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Sorghum bicolor
                                    Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M.
                                                                                                                               Sorghum bicolor
                                                                                                                                                   sorghum
                                                                                                                                                                                          BE597204.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .L.H.
An EST database from Sorghum: dark-grown seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 404)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
EST database from Sorghum: pathogen-induced plants
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706 583 0210
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a 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhOI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
127 c 122 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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                                                                                                                                                                                        GI:9852179
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core 76; DB
Pred. No. 0;
Mismatches
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n 1 (DG1) Sorghum bicolor
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                                      Pratt
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RESULT 9
BE362317
LOCUS
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                                                                                                                                                                                                                                                                        VERSION
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Best Local S
Matches 76
                                                              TITLE
                                            JOURNAL
                                                                                                    AUTHORS
                                                                                                                                                                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGCAGTACAGCGCCA 892
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and I
                                                                                                    Cordonnier-Pratt, M.-M.,
                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 471)
                                                                                                                                                                                                         Sorghum bicolor
                                                                                                                                                                                                                                                                                                                         BE362317
DG1_85_C06.g1_A002 Dark Grown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Cordonnier-Pratt MM
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Sequences have been trimmed
below Phred quality 16. The
                                                            An EST database from Sorghum:
                                                                                                                                                                                                                           sorghum.
                                                                                                                                                                                                                                                                        BE362317.1
                                                                                                                                                                                                                                                                                               BE36231
                                                                                                                                                                                                                                                                                                                sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //clone_lib="Pathogen induced 1 (PII)"
//clone_lib="Pathogen induced 1 (PII)"
//clone_lib="Pathogen induced 1 after insculation;
/mote="Organ: Anthraconose-infected leaves from
two-week-old sorghum plants 48 hr after insculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Collectrichum graminicola, which is a sorghum isolate)
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthraconose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WarXINIG; While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."

97 a 135 c 127 g 77 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76; DB; Pred. No. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                    Gingle, A.,
  Bioinformatics
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                                                                                                                                                                                                                                                                                                                                  n 1
dd
                                                            dark-grown seedlings
                                                                                                                                                                                                                                                                                                                                  mRNA linear ES
(DG1) Sorghum bicolor
                                                                                                    Marsala,C.,
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                                                                                                       Sudman, M.
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                                                                                                                                                                   Tracheophyta;
aceae; PACC
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                                                                                                                                                                                                                                                                                                                                       cDNA, mRNA
                                                                                                       and Pratt
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JOURNAL COMMENT
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BE597234
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SOURCE
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VERSION
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ORIGIN
                                                       FEATURES
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                     High quality sequence start: 4 High quality sequence stop: 443
                                                                                                                                                                Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                     Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                       Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 471)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE597234 471 bp mRNA 1 PI1_69_G08.g1_A002 Pathogen induced 1 (PI1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 40 High quality sequence stop: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: PolyTMix
                                                                                                                            Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                    An EST database from Sorghum: pathogen-induced plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sorghum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE597234.1
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nt Sciences Building, Rm.
: 706 542 1860
: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoR; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 147 c 134 g 84 t
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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m. 2502, Athens, GA 30602-7271,
                                                                                                                                                                to exclude PolyA, vector and regions threshold for highest quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 18-AUG-2000
bicolor cDNA,
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JOURNAL
COMMENT
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BM318212
LOCUS
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ORGANISM
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В

LOCUS

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121
                                                        /clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after incculation;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM41 of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves hrvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
the nathorsen "
    pathogen.
128 c
131 g
    91 t
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCAGTACAGCGCCA
                                                                                                                                                  Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                     Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM318212
P11 79_G11.g9_A002 Pathogen
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pcaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                       High quality sequence start: 3 High quality sequence stop: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    An EST database from Sorghum: pathogen-induced plants
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ilarity 100.0%;
Conservative (
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                              Location/Qualifiers
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gen induced 1 (PI1)
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) Sorghum
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bicolor cDNA,
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/clone_lib="Pathogen induced 1 (PI1)" /note="Organ: Anthracnose-infected leaves from

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817 CGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTG 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCAGTACAGCGCCA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 512)
Cordonnier Pratt, M.-M., Gingle, A., Marsala, C. and P
An EST database from Sorghum: light-grown seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences have been trimmed below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYA-Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW672196.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   two-week-old sorghum plants 48 hr after inoculation; vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; Two-week-old sorghum plants (BTX 623 cultivar) were infected with pathogen (isolate FRM42I of colletotrichum graminicola, which is a sorghum isolate) RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
/note="Organ: 10- 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                     organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 g
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Pred. No. 0;
Mismatches
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RESULT 12 AW672196

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BE600412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 566)
1 (bases 1 ro 566)
2 rudonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum bicolor
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_96_A03.gl_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
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153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706 542 1860
706 583 0210
                                                        /organism="Sorghum bicolor"

/db xref="taxon:4558"

/clone_llb="Pathogen induced 1 (PII)"

/clone_llb="Pathogen induced 1 (PII)"

/note="Organ: Anthracnose-infected leaves from

/note="Organ: Anthracnose-infected leaves from

two-week-old sorghum plants 48 hr after inoculation;

vector: pBluescript II from Lambda Zap II; Site_1: Xho;

Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)

cultivar) were infected with pathogen (isolate FRM42I of

Colletotrichum graminicola, which is a sorghum isolate).

RNA was prepared from infected leaves harvested from 45

seedlings 48 hours after inoculation. Note: young

seedlings (2 weeks old) exhibit juvenile resistant

reaction, which is an incompatible interaction. As they

grow older (4 weeks or older), plants resume susceptiblity

to anthracnose disease. The library was made from poly-A

RNA in the cloning vector lambda ZAP II. Clones to be

sequenced were prepared by mass excision. WARNING: While

most or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                        plant,
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pathogen."
149 c 1
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                                      no effort was made to eliminate ESTs deriving from
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Pred. No.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 570)
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE597297 570 bp mRNA linear EST 18-AUG:20
PI1_71_G06.g1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 37 High quality sequence stop: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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                         Similarity
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5.6%; Score 76; DB ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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                                                                                                               /organism="Sorghum bicolor"
//db_xref="taxon:4558"
//clone_ilb="Pathogen induced 1 (PII)"
//clone_ilb="Pathogen induced 1 (PII)"
//clone_ilb="Pathogen induced 1 (PII)"
//note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda Zap II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."
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Query Match Best Local

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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                        Query
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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                          AAB99738
ABB93359
AAB16437
AAB99741
AAB1648217
AAB99746
AAB99746
AAB99743
             AAB16426
                                                                                                                                                                                                                                                                                              SUMMARIES
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Oryza sativa perox
Herbicidally activ
Pinus radiata pero
Oryza sativa perox
Pinus radiata pero
Stylosanthes humil
Oryza sativa perox
Herbicidally activ
Oryza sativa perox
Eucalyptus grandis
                                                                                                                                                                                                                             Description
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Arabidopsis thalia	736	21	328	5	N	45
icidally	9354	23	321	Ġ	N	44
idopsis	AAG17363	21	321	ŗ	N	43
oybean seed	4493	19	352	5	27.	42
ybean s	7313	19	352	5		41
ST	0881	21	285	ŗ	28.	40
opsis	50	21	356	9	39.	39
icidally	97	23	336	9	39.	38
bidopsis	AAG41501	21	336	9	39.	37
bicidally	37	23	358	7.	53.	36
idopsis	7	21	358	7.	55.	ω 5
icidally	37	23	335 35	7.	65.	34
opsis	54	21	335	8	71.	ω
Lγ	78	23	337	8	7	32
opsis	51	21	337	œ	7	3 1
dopsis	80	21	346	8	7	30
iata pe	3	21	287	ف	9	29
bicidally	78	23	338	٥	0	28
idopsis	2	21	338	9	0	27
œ	131	21	338	٥	0	26
Ferbicidally activ	100	23	315	9.	0	25
icidally	326	23	331	Ò.	0	24
er	974	22	326	0	\vdash	23
icidally	100	23	321	0		22
יט כדי	7899	23	311	۳	\rightarrow	21
e Per5 root p	8789	20	333	÷	N	20
us radiata per	1644	21	266	Ö	84	19
s thal	AAG14575	21	309	ښ.	63	18
bidopsis thal	1457	21	308	Ü.	63.	17
idopsis thal	4911	21	309	4	66.	16
bidopsis tha	49	21	308	4	66.	15
abidopsis thal	457	21	316	٠.	67.	14
bicidally act	9386	23	316	Ä	70.	13
dopsis thal	4911	21	316	54.3	870.5	12
za sativa	AAB99744	22	320	Ġ	85.	11

ALIGNMENTS

RESULT 1 AAB99738

WPI; 2001-381695/40. N-PSDB; AAH44077. Ohashi Y, Mitsuhara I, Hiraga S; 10-DEC-1999; 08-DEC-2000; 2000WO-JP08728 WO200142475-A1 Oryza sativa; rice; peroxidase; POX; characteristic; gene expression; modification; plant; bacterial infection; Magnaporthe grisea. Oryza sativa peroxidase s4235 protein SEQ ID NO:14. 12-SEP-2001 (first entry) AAB99738; AAB99738 standard; (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES 14-JUN-2001. 99JP-0352472 Protein; Sasaki T, 327 A Nagamura Y, Ito Η, Iwai T;

New set of rice peroxidase genes for in rice under varying conditions and

analysis of peroxidase expression production of rice plants with

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ARESULT 2
ARB93359
ID ARB9
XX ARB9
AC ARB9
XX ARB9
XX ARB9
XX Herb
XX Herb
XX Herb
XX Herb
XX WO20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AnH44071 to AnH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the Experoxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene CC expression analysis. The set of genes are used for the analysis of the CC pattern of peroxidase gene expression in particular rice plants and CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea. CC The present sequence represents a rice peroxidase encoded by a gene from CC the gene set described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
28-AUG-2001; 2001WO-EP09892.
                                                                                          W0200210210-A2
                                                                                                                                                                                  Herbicidal;
                                                                                                                                                                                                                               Herbicidally active polypeptide SEQ ID NO 2570.
                                                                                                                                                                                                                                                                                                                                                                       ABB93359 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 155-157; 258pp; Japanese.
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                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                               31-MAY-2002
                                                                                                                                                                                                                                                                                                                            АВВ93359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 TNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VAVSLLSCVAHAQLSPTEYASSCPNLQSIVRAAMTQAVASEQRMGASLLKLEFHDCEVQG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQIRRNCRVVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLLSRRGLFHSDQELF----NGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLLTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VALAVVFLAAEAQLSPGYYNATCPGVVSIVRRGMAQAVQKESRMGASILRLFFHDCFVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEVRINCRRVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTVGWARCSTERTHIYNDTGVNATFASQLRTKSCPTTGGDGNLAPLELQAPNTFDNAYFT. 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTIGQARCTTFRGRIYGDTDINASFAA-LRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNLLGGPNWTVPLGRRDARTTSQSAANTNLPPPGASLASLLSMFSAKGLDARDLTALSGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKAQLEASCKATVSCADIITLAARDA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327
                                                                                                                                                                                  plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313
                                                                                                                                                                                  agriculture;
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                                                                                                                                                                                                                                                                                                                                                                         324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                    herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plants sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
WO200022099-A1
                                                           plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
Pinus radiata; Monterey pine.
                                                                                                     Pinus radiata peroxidase protein sequence SEQ ID NO:389
                                                                                                                                       24-OCT-2000
                                                                                                                                                                                                   AAB16437 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; SEQ ID NO 2570; 261pp + Sequence Listing; English.
                                                                                                                                                                      AAB16437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-269010/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                      171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                        181 SAVGLSTRDMVALSGAHTIGQSRCTNFRARIYNETNINAAFATTRQRTCFRASGSGDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GYVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GASILRLFFHDCFVNGCDGSILLDDTSSFTGEQNAAPNRNSARGFNVIDNIKSAVEKACP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASPTLMQCLVAVSLL-----SCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASNKLISILVLVVTLLLQGDNNYVVEAQLTTNFYSTSCPNLLSTVQTAVKSAVNSEARM 60
                                                                                                                                                                                                                                                                                                                                                                                                                       APIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVSCADILAIAARDSVVALGGPNWNVKVGRRDARTASQAAANSNIPAPTSSLSQLISSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GASLLRLFFHDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACP
                                                                                                                                                                                                                                                                               IKMGDISPLTGSSGEIRKVCGRTN 324
                                                                                                                                                                                                                                                                                                            IRMGNVGVLTGTAGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                            APLDYTTAASFDNNYFKNLMTQRGLLHSDQVLFNGGSTDSIVRGYSNNPSSFNSDFTAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                      (first entry)
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61.4%;
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                                                                                                                                                                                                      318
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Pred. No. 6.1e-89;
6; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 12;
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The present invention describes isolated polynucleotides and proteins CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), CC commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (CCR), phenylalanine ammonia-lyase (PAL), Cinnamyl-COA reductase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-commarate:COA ligase (ACL), CC coniferol glucosyl transferases (CGT), coniferol plucosylase, ferulate-5-hydroxylase (F5H), alpha-amylase, CC caffeic acid methyl transferase, caffeoyl COA methyl transferase, CC commerate COA ligase, cytochrome p450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, cytochrome p450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC composition and the structure of a plant, especially eucalyptus and pine CC species, and for modifying the activity of an enzyme involved in lignin CC species, and for modifying the activity of an enzyme involved in probes CC and primers useful for detecting similar DNA and RNA sequences in any cransism and for DCP amplification. The lignin content can be efficiently
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and primers useful for detecting similar DNA and RNA sequences in any organism and for PCR amplification. The light content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB1341 to AAB16449 represent polynucleotide and protein sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and the species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LID. (FLET-) FLETCHER CHALLENGE FORESTS LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-2000
    301
                                                                                                                                                    181
                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                         59
    SPLTGTNGQIRKNCRKSN 318
                                                                                              CADILALAARDGTNLLGGGTTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQG
                                                                                                                                                                                                                                                                                                                     LRLFFHDCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVS 114
                                                                                                                                                                                                                                                                                                                                                                                           MQCLVAVSLLSC-----VAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASL 58
                                      GVLTGTAGQIRRNCRVVN 312
                                                                                                                                                                                                                           CADILTIAARDSIVELQGPTWTVMLGRRDSTTASLSAANNNIPSPASSLSTLISSFQAHG
                                                                                                                                                                                                                                                                                                 VRLHFHDCFVNGCDGSILLDDNATFTGEKTAGPNANSARGFEVIDSIKTQVEAACSGVVS
                                                                                                                                                                                                                                                                                                                                                                       MRTLVCIGLMAVEVAFIHINAVNGQLSSTFYAKSCPRLPSIVKSVVKQAVAKEKRMGASL 60
                                                                                                                                                  LSTKDLVALSGAHTIGQSRCAFFRTRIYNETNINAAFATSVKANCPSAGGDSNLSPLDAV
                                                                                                                                                                    LSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQ
                                                                      TSITEDNKYYSNLKIQKGLLHSDQQLFNGGSTDSQVTAYSSNQNSFFIDETAAMVKMGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Page 199; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0169789.
99US-0143811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-NZ00168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.2%;
60.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 965; DB 21;
Pred. No. 1.9e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                        300
                                                                                                            294
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                                                                                                                                                240
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                                                                                                                                                                                                                                                             174
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AAB99741
                                    Db
                                                                  QΥ
                                                                                                          B
                                                                                                                                            Qy
                                                                                                                                                                                                                                                             DXXXI
                                                                                                                                                                                    Matches 189;
                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohashi Y,
Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa; modification;
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-2000; 2000WO-JP08728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB99741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB99741 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH44080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-381695/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200142475-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2001
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1999;
                                    61
                                                                      52
                                                        QRMGASLLRLFFHDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEA 107
ACPGVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLI 167
                                    KRIGASIVRLFFHDCFVQGCDASLLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVET 120
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitsuhara
                                                                                                                                                                                                                                                             327 AA;
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peroxidase r3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                    59.5%;
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                                                                                                                                                                                46;
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The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are given in AnH44071 to AnH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene cc expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and CC pattern of peroxidase gene expression in particular rice plants and CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea.

The present sequence represents a rice peroxidase encoded by a gene from the gene set described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with desired characteristics \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 174-176; 258pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
                                       MAQPTWSARRVTAALVVMVVVVLAVAGGSWAQLSPSFYSYSCPGVFNAVKRGMQSAIARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki T,
                                                                                                                                           Score 954.5; DB 22;
Pred. No. 2.1e-86;
6; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
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                                                                                                                                                                                                               DB 22;
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                                                                                                                                               Indels
                                                                                                                                                                                                               Length 327
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The present invention describes isolated polynucleotides and proteins commarate 3-hydroxylase (C3H), phenolase (PML), O-methyl transferase (C4H), counsarate 3-hydroxylase (C3H), phenolase (PML), O-methyl transferase (CMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-counsarate:COA ligase (4CL), CC coniferol glucosyl transferase, (CGT), coniferon beta-glucosidase (CBC), CC caffeic acid methyl transferase, caffeoyl cOA methyl transferase, CCC counserate COA ligase, cytochrome P450 LXALA, diphenol oxidase, flavanol CC counserate COA ligase, cytochrome P450 LXALA, diphenol oxidase, flavanol CC counserate COA ligase, cytochrome P450 LXALA, diphenol oxidase, flavanol CC counserate COA ligase, cytochrome P450 LXALA, diphenol oxidase, flavanol CC counserate COA ligase, plavanoid hydroxylase, and isoflavone reductase, CCC which are involved in the lignin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC content, composition and structure of a plant having altered lignin CC content, composition and structure. They can be used for designing probes CC and primers useful for detecting similar DNA and RNA sequences in any creations and for PCR amplification. The lignin content can be efficiently condified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; lignin;
Pinus radiata;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pinus radiata peroxidase protein sequence SEQ ID NO:395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB16443 standard; Protein; 323
                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 202-203; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-317962/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNLAPLDLQTPTVFENNYYKNLVVKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGMIKMGDITPLTGSNGEIRKNCRRIN 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAMIRMGNVGVLTGTAGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNLAPIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lignin biosynthetic pathway; Eucalyptus grandis; Monterey pine.
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99US-0143811.
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         PTTTRACTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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     plant cell transformed with Stylosanthes humilis Shpx6 peroxidase useful to confer on plants resistance to fungi, e.g. Phytophthora parasitica, Leptosphaeria maculans or Sclerotinia sclerotorium
                                                                                                                                                                                                                                                                                                                                                                                                       Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW38217 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                   WPI; 1997-549739/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stylosanthes humilis Shpx6 peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-1998
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                                                                                     N-PSDB;
                                                                                                                                         Goulter KC,
                                                                                                                                                                                                                                                                                                                                                   W09741237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stylosanthes
                                                                                                                                                                                                                                       29-APR-1996;
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                                                                                                                                                                                                                                                                                                               06-NOV-1997.
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                                                                                     AAT95782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                         Kazan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               humilis strain Paterson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                       96AU-0009532.
                                                                                                                                                                                                                                                                         97WO-AU00253
                                                                                                                                                                                                                                                                                                                                                                                     /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide and protein sequences used the present invention.
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Peroxidase; Shpx6; transgenic plant; fungus resistance; disease protection; Phytophthora parasitica; Leptosphaeria maculans; Sclerotinia sclerotorium. (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY (GRAI-) GRAINS RES & DEV CORP. 181 TALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRS--GGDGNLAPIDVQTPVR 10 CIAVMVFIVCSITDTVNGQLSSTFYDKSCPTALSVVKAAVKQAVANEKRMGASLLRLHFH 9 CLVAVSLLSC----VAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFH VALSGGHT IGQAQCKNFRAH I YNETNIDSAY AT SLRSKCPSTTGSGDSNLSPLDYMTPTV FDKNYYSDLKSQKGLLHSDQELFNGGSTDSQVTTYASNQNTFFSDFAAAMVKMGNIKPLT IAARDSVYELGGPSWTVMLGRRDSTTASKSGANSNIPPPTSSLSNLISLFQAQGLSAKEM DCFVNGCDGSVLLDDSSTITGEKTANPNANSARGFDVIDTIKSNVEKACSGVVSCADILA DCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILA 120 FDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLT Score 950; DB 21; Pred. No. 5.9e-86; Length 323; 10; Gaps 298 238 69 64 189 249 309 Ψ

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RRESULT 7
ARB99176
ID ARB9
XX ARB9
XX ARB9
XX ARB9
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XX OTYZ
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XX MOC1
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Best Local Simi
Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter) and a Shpx6 DNA sequence (see AAT95782), or a hybridising sequence or fragment that encodes an enzyme with peroxidase activity. Also claimed are plant cells harboring the DNA construct, a plant comprising such cells, and material from such a plant, especially seed, pollen, a stem segment or a cutting. Resistance to fungi, especially phytophthora parasitica, reptosphaeria maculans or Sclerotinia sclerotorium, can be conferred on cereal, legume, oilseed, sugar or fibre plants, particularly maize, banana, peanut, field pea, sunflower, tomato, canola, tobacco, wheat, barley, oat, potato, soybean, cotton,
                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa peroxidase r2576 protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This protein comprises the Shpx6 peroxidase of Stylosanthes
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                                                                                                                                                                                                                                                                                                            Oryza sativa; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carnation
                                                              08-DEC-2000; 2000WO-JP08728
                                                                                                                                                                                                                                                 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB99746;
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      10-DEC-1999;
                                                                                                                             14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVQGCDASVLLDDTSNFTGEKTARPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGYYKNLLVKKGLFHSDQQLFNGGSTDSQVNGYASNPSSFCSDFGNAMIKMGNISPLTGS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARDSVVALGGPSWTVQLGRRDSTTASLSLANSDLAAPTLDLSGLISAFSKKGLSTSEMVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLIILVMSLIG-LGSGQLSSNFYATTCPNALSTIRSGVNSAVSKEARMGASLLRLHFHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGQIRTNCRKTN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                         rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.48;
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; Pred. No. 1.3e-84;
41; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                         NO:30.
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RESULT 8 ABB93867

ABB93867 standard; Protein; 325

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31-MAY-2002 ABB93867;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC in the sample plant; and (4) DNA microarrays for peroxidase gene expressed CC expression analysis. The set of genes are used for the analysis of the CC expression analysis. The set of genes are used for the analysis of the middle component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC peroxidase gene expression to impart particular characteristics to the CC plants such as response to bacterial infection by Magnaporthe grisea.

CC The present sequence represents a rice peroxidase encoded by a gene from CC the described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohashi Y,
Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with desired characteristics \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 205-207;
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302
                                   300 TAGQIRRNCRVVN 312
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                                                                                                                                                                                                                                                                                                                                                  62 FFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILAL
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                                                                                                                                                                                                                                                                                                           HEHDCEYQGCDASVLL-SGQEQNAGPNAGSLRGENVVDNIKTQVEAICSQTVSCADILAV
                                                                                                                                                                                                                                                                                                                                                                                                              ASPTLMQCLVAVSLLSCYAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRL 61
                                                                                              DTAYETNILISRRGLEHSDQELENGGSQDALVRQYSASASLENADEVAAMIRMGNVGVLTG
                                                                                                                                                                             ALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGDGNLAPIDVQTPVRF 239
                                                                                                                                                                                                                                  AARDSVVALGGPSWTVLLGRRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDMV
                                                                                                                                                                                                                                                       AARDGINLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMT
                                                                                                                                                                                                                                                                                                                                                                                         ASSYSLMLLVAAAMAS-AASAQLSATFYDTSCPNALSTIKSAVTAAVNSEPRMGASLVRL
TQGQIRLNCSKVN 314
                                                                            DSAYYTNLLSNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKMGNISPLTG
                                                                                                                                                      ALSGAHTIGQAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   set described above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 926; DB 22;
Pred. No. 1.4e-83;
12; Mismatches 82;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 3078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tjetjen K, Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP09892
  AAB99743;
                             AAB99743 standard; Protein; 326
                                                                                                  316
                                                                                                                             303
                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                     136
                                                                                                                                                                                                                                            185
                                                                                                                                                                                                                                                                                                                                                                                                          10 LVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQ 69
                                                                                                                                                                                                                                                                                                                             76
                                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-269010/31
                                                                                                                                                                                                                             GAHTIGQARCTTERGRIYGDTDINASEAALRQOTCERS--GGDGNLAPIDVQTEVREDTA 242
                                                                                                                                                                                                                                                                                     GTNLLGGPTWSVPLGRRDSTTASASLANSNP-PPPTASLGTLISLFGRQGLSPRDMTALS 184
                                                                                                                                                                                                                                                                                                                                          GCDGSILLDAG----GEKTAGDNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAÄRD 125
                                                                                                                                                                                                                                                                                                                                                                                QIRRNCRVVN 312
                                                                                                                                                                        YFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAG
                                                                                                                                                                                                                                                                     SVLLMGGRGWSVKLGRRDSITASFSTANSGVLPPPTSTLDNLINLFRANGLSPRDMVALS
                                                                                                                                                                                                                                                                                                                           GCDASILLDDTRSFLGEKTAGPNNNSVRGYEVIDAIKSRVERLCPGVVSCADILAITARD
                                                                                                                                                                                                                                                                                                                                                                                                                                        187;
                                                                                                 QIRRSCRRPN
                                                                                                                                                       YFMQLVNHRGLLTSDQVLFNGGSTDSIVVSYSRSVQAFYRDFVAAMIKMGDISPLTGSNG
                                                                                                                                                                                                              GAHTIGQARCVTFRSRIYNSTNIDLSFALSRRSCPAATGSGDNNAAILDLRTPEKFDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 912.5; DB 23;
Pred. No. 3.2e-82;
""matches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 3078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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В Q

193

LAALSGAHTVGRASCVNFRTRVYCDANVSPAFASHQRQSCPASGGDAALAPLDSLTPDAF

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The present invention describes a set of peroxidase genes found in CC plants, especially rice, and their homologues, modified forms and CC fragments, where the sequences of the peroxidase genes in the set are CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the CC control of the gene set; (2) the preparation of cassette vectors using CC the genes and promoters; (3) analysis of plant characteristics using the CC peroxidase set by isolating RNA from the plant, binding the RNA to a CC membrane, mixing with a labelled peroxidase gene set, incubating, and CC detecting the label signal to show which genes in the set are expressed CC in the sample plant; and (4) DNA microarrays for peroxidase gene CC expression analysis. The set of genes are used for the analysis of the CC pattern of peroxidase gene expression in particular rice plants and CC their component tissues and under different environmental conditions, CC and modification of rice plants to provide desired specificities of CC plants such as response to bacterial infection by Magnaporthe grisea. CC The present sequence represents a rice peroxidase encoded by a gene from the gene set described above.
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                                           Вþ
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                                                                                                                                                                                                                                 Matches 170;
                                                                                                                                                                                                                                                      Query Match
Best Local :
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Hiraga S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200142475-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New set of rice peroxidase genes for analysis of peroxidase expression in rice under varying conditions and production of rice plants with \cdot desired characteristics \dot{\,}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 186-188; 258pp; Japanese.
                                                                                                                                                                                                                                                                                                    Sequence
                                             133
                                                                             120
                                                                                                           73
                                                                                                                                           65
                                                                                                                                                                         13
                                                                                                                                                                                                       0
                                                                                                                                                                                                    LMQCLVAVSL-LSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-381695/40
                                                              ALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRD 179
                                                                                                         DCFVGGCDASVLLDDTPAAPGEKGVGPNAVGSTTVFDLVDTIKAQVEAVCPATVSCADVL
                                                                                                                             DCFVQGCDGSILLD----AGGEKTAGPN-LNSVRGFEVIDTIKRNVEAACPGVVSCADIL 119
                                                                                                                                                                       LLLLLLAVALALAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFYH
MTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRF
                                             AIAARDSVNLLGGPSWAVPLGRRDALSPSRSAVSTDLPGPEADISALVSAFAAKGLSSRD
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitsuhara
                                                                                                                                                                                                                                                                                                       326 AA;
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peroxidase s10927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-JP08728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0352472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peroxidase; POX; characteristic; gene expression;
; bacterial infection; Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I,
                                                                                                                                                                                                                                                        56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki T,
                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                       Score 901; DB 22; Pred. No. 4.5e-81; 1; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO:24
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                                                                                                                                                                                                                                                                       Length 326;
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Matches

180;

46;

Mismatches

85;

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Gaps

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RESULT 10
AAB16426
ID AAB16
XX AAB16
XX AAB16
XX PAB16
XX Plant
XW Plant
XW Plant
XW Pinus
XX Pi Bloks
XX Claim
XX Cl
                                                                                                                                                                               The present invention describes isolated polynucleotides and proteins CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (CMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC caffeic acid methyl transferase, caffeoyl COA methyl transferase, CC coumerate COA ligase, cytochrome P450 LIXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC polynucleotides can be used for modulating lignin content, lignin CC content, composition and structure. They can be used for designing probes CC and primers useful for detecting similar DNA and RNA sequences in any CC confished using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AXB16449 represent polynucleotides and protein sequences used in the CC exemplification of the present invention.
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 193; 213pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathway useful fo
and pine species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-317962/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis; Pinus radiata; Monterey pine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTAYFINLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTG
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99US-0143811.
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56.1%;
57.0%;
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Query Match Best Local Similarity

Score Pred.

899.5; DB 2 No. 6.1e-81;

21;

Length 315;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AnH44071 to AnH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed
                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa; modification;
                                                                                                                                                                           desired
                                                                                                                                                                                                    New set
                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000; 2000WO-JP08728
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200142475-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB99744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB99744 standard; Protein;
                                                                                                                                                                                                                                                                                                                  (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
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DB; AAH44083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVGFSVVVVLLATSVIT-TARCKLSPSHYQSTCPKALSIVRAGVAKAIKNETRTGASLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFFDNLYYHNLLQKKGLLHSDQELFNGSSVDSLVKKYACDTGKFFRDFAKAMIKMSEIKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKNMVALSGSHTIGLARCTSFRRRIYNDSNIDTSFAHKLQKICPRIGNDSVLQRLDIQTP
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                                                                                                                                                                                      of rice peroxidase genes
under varying conditions
                                                                                                                                                                          characteristics
                                                                                                                                                                                                                                                                                         Mitsuhara
                                                                                                                                            Page 192-194; 258pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peroxidase s14493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; POX; characteristic; gene expression; infection; Magnaporthe grisea.
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RESULT 12
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08-APR-1999

16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea. The present sequence represents a rice peroxidase encoded by a gene from the gene set described above.
                                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                              EP1033405-A2.
                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 62095.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTGAHTVGVAQCTNFRSRLYGESNINAFFAASLRASCPQAGGDTNLAPLD-STPNAFDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAVSVLVVALAAAASGQLSTTFYASSCPTALSTIRSAVNAAVAREPRMGASLLRLHEHDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFTDLIAGRGLLHSDQELYRGDGSGTDALVRVYAANPARFNADFAAAMVRMGAIRPLTGT
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Similarity 57.4%;
79; Conservative '
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 990S-0121825
990S-0123180
990S-0125748
990S-0125786
990S-0126766
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990S-0127462
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990S-012834
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Pred. No. 1.5e-79;
46; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length
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promoter;
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30-APR-1999;
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990S-0132484

990S-0132484

990S-0132485

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990S-013425

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99US-0144335 99US-0144352 99US-0144814 99US-0144814 99US-0145086 99US-0145085 99US-0145085 99US-0145085 99US-0145087 99US-0145087 99US-0145087

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990S-0145951 990S-0146386 990S-0146389 990S-0147008 990S-0147204 990S-0147302 990S-0147303 990S-0147333 990S-0147333 990S-0147443 990S-0147493 990S-0147493 990S-0148341 990S-0148341

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RESULT 13
ABB93866
ID ABB93
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AC ABB93
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Best Local Similarity 57.:
Matches 177; Conservative
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28-AUG-2001; 2001WO-EP09892.
                                                07-FEB-2002
                                                                                        WO200210210-A2
                                                                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                 Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                               Herbicidally active polypeptide SEQ ID NO 3077.
                                                                                                                                                                                                                                                                            31-MAY-2002
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Pred. No. 4.7e-78;
4; Mismatches 82; Indels 7;
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3-0150884 3-0150884 3-0151066 3-0151066 3-0151066 3-0151303 3-0151303 3-01513303 3-0153133 3-0153758 3-0154018 3-0154018 3-0154018 3-0155403 99US-0149426. 99US-0149722. 99US-0149723.

-0149929 -0149902 -0149930

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                         AAG14574 standard;
          Arabidopsis thaliana
                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 14489.
                                                                                                17-OCT-2000
                                                                                                                     AAG14574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER AG
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                              termination sequence.
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Search completed: April 26, 2003, 12:33:32 Job time: 78 secs

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ALIGNMENTS

	JOURNAL COMMENT	TITLE	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	LOCUS DEFINITION	RESULT 1 AA979912
Schnable laboratory Iowa State University G405 Agronomy, Ames, IA 50011, USA Tel: (515)-294-0975 Fax: (515)-294-2299 Email: schnable@iastate.edu PCR PRimers FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3') BACKWARD: Ty71 (5'-TRATACGACTCACTATAGGGC-3') Plate: MEST3 row: D column: 6 Seq primer: tw1412 (5'-GAAGATACCCCACCAAACC-3').	Unpublished (1997) Contact: Schnable, PS	Wen, T.J., Ashlock, D.A. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings	1 (bases 1 to 848)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andronoconeae; Jea	Zea mays	Zea mays.	EST.	AA979912.1 GI:3157290	sequence. AA979912	AA979912 848 bp mrna linear EST 26-MAY-1,998 MEST3-D6.TW1412.Seq ISUM2 Zea mays cDNA clone MEST3-D6 5', mRNA	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 CCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAG 384
    985 AACTGCCGGGTCGTCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACTTCACCAAC 804
                                                                                                                                                                                                                                                                                       ATCAACGCCTCCTTCGCGGCGCTGCGGCAGCAGACGTGCCGCGGTCCGGCGGCGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGGCGGACAGATCAGGCGC
                                                                                                GACGCGCTGGTGAAGCAATACAGCGCCCAGCGCCTNGCTCTTCAACGCCGACTT-GTGGCA
                                                                                                                                                                              CTGCTGTCGCGGGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAG 864
                                                                                                                                                                                                                                                                                                                                                     CACACCATCGGGCAGGCCCGGTGCACCACCTTCCGCGGCCGCATCTACGGCGACACCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTCCCTGTTCGGCAGGCAGGGCCTGTCGCCGCGACATGACGGCGCTGTCGGGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTCCCTGTTTCGGCAGGCAGGGCCTGTCGCCGCGACATGACGGCGCTGTCGGGCGCG 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAGCGCCTCGCCAACAGCAACCTCCCGCCCCGACGGCCAGCCTCGGCACGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGCGCTGGTGAGGCAGTACAGCGCCAGCGCCTCGCTTCAACGCCGACTTCGTGGCA 924
                                                                                                                                                               CTGCTGTCGCGGANGGGCCTGTTCCACTCGGACCANGAGCTCTTCAACNGCGGGTCGCAA 540
                                    ACCATGATTANGATGGG-AACCTTTGGGTGCTCAACCGGACCGTTGG-NAGATCAAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /notes "Organ: green seedlings; Vector: pAD-GAL4; Site_1: ECORI; Site_2: XhoI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNAse H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybrilAP lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
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/cultivar="B73"
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95.78;

 Mismatches

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Pred. No. 1.1e-81;
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Best Local
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    634
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GTGAACCCCTTTCGCGGNNGGNAATTTATGNGACCNAAACATNAACGCCTCCCTTCTNGG
                                                                                                                                                                                                        TGCACCACCTTCCGCGGCC-GCATCTACGGCGACACCGACATCAACGCCT-CCTTCGCGG 703
                                                                                                       CTGTCGCCGCGC---GACATGACGGCGCGTGTCGGGCACGCACACCATCGGGCAGGCCCGG 645
                                                                                  CTNTCCCCCCCCCNGAAAANTAAGGCGCTNTCGGGGGCGNACACNNATGGGCAGGGCCGG
                                                                                                                                                                                                                                                      652;
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AI374530.1
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MEST3-D6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G405 Agronomy, Ames, IA 50011, Tel: (515)-294-0975 Fax: (515)-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: T7-XJ (5'-TAATACGACTCACTATAGGGC-3')

Plate: MEST3 row: D column: 6

Seq primer: POLXT-N (5'-TITTTTTTTTTTTTTTTTTTTTTTT(AGC)-3').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 850)
Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings
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BACKWARD: T7-YJ (5'-TAATACGACTCACTATACCCC-3
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                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                   /note-Norgan: green seedlings; Vector: pAD-GAL4; Site_1: /note-Norgan: green seedlings; Vector: pAD-GAL4; Site_1: /note-Norgan: green seedlings; Vector: pAD-GAL4; Site_1: /note-Norgan: green seedling das collabored from oligo-dr follows. First-strand cDNA was prepared from oligo-dr follows. RNA by priming with an XhoI oligo-dr primer. The resulting DNA:RNA hybrid was treated with RNAse H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybridaP lambda vector (Stratagene) and excised as pAD-GAL4 phagemids. "

(Stratagene) and excised as pAD-GAL4 phagemids."
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.POLYT-N.Seq ISUM2 Zea π
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/dev_stage="Two-leaf-stage green se
/lab_host="XL1-MFR Blue"
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/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                         Score 537.6; DB 9;
Pred. No. 1.6e-71;
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AW671673
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                       is 20.
Seq primer: JEN REV
High quality sequence s
POLYA-No.
                                                                                                                                                                                                              sorghum.
Sorghum bicolor
Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACC.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC.
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 633)
                                                                                                                                                                                                                                                                                                                                                     sequence.
AW671673
                                                                              Email: mmpratt@uga.edu
Sequences have been tri
below Phred quality 16
                                                                                                                                              Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                      Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. An EST database from Sorghum: light-grown sees Unpublished (2000)
Contact: Cordonnier-Pratt MM
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AW672124
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Best Local :
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                                                                                sequence.
AW672124
AW672124.1
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                     EST.
                                                       sorghum
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В

FOCUS

δÃ 밁 20 망

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CAAGCGGAACGTCGAGGCCGCGTGCCCCGGCGTCGTGTCGTGCGCCCGACATCCTCGCGCT
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                                                                                                  CTACGGCGACACCAACATCAACGCC
                                                                                                                                   CTACGGCGACACCGACATCAACGCC
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AW672124 (
LG1_357_F02.b1_A002 Light
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14 day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
a 230 c 190 g 108 t
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91.2%;
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2.3e-71;
hes 55;
   mRNA
(LG1)
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       bicolor cDNA, mRNA
                   EST 19-JUL-2000
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                                                                                                                                                                                                                                                                                                                          CTGCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGC 231
                                 TCGCCGCGCGACATGACGGCGCTGTCGGGCGCGCACCATCGGGCAGGCCCGGTGCACC
                                                                                GCCGACATCCTTGCCCTTGCCGCGCGAGACGGAACCAATCTGCTCGCCGGGCCGACCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGTGCAGGTTGCCATGGCGGCTCCTACCTTGATGCAATGCTTGGTCGCCATTTCCCTC 73
                                                              AACGTGCCGCTGGGCCGGCGGACTCGACGACGGCAAGCGCGTCCCTTGCCAACAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 625)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USI
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
Sequences have deanity 16. The threshold for highest quality sequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: JEN REV
High quality sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4558"
/clone_lib="flight Grown 1 (LG1)"
/clone_lib="flight Grown 1 (LG1)"
/note="forgan: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Eco
; The library was made from poly-A RNA in the cloning
vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."
233 c 188 g 110 t 2 others
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613
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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BG842311
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                         737 GCGACGCCAACCTGGCGCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACT 796
                                                                    677 ACACCGACATCAACGCCTCCTTCGCGGCGCTGCGGCAGCAGACGTGCCCGCGGGTCCGGGC 736
 61
                                                        1 ACACCGACATCAACGCCTCCTTCGCGGCGCGCTGCGGCAGCAGACGTGCCCGCGGTCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTTCCGCGGC
sequence.
BG842311
BG842311.2
EST.
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iowa State University
G405 Agronomy, Iowa State University,
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
On May 25, 2001 this sequence version replaced g1:14208633
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pcaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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MEST29-D08.T3
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qiu.F., Cui.F., Guo.L., Ashlock.D.A, Wen.T.J. and Schnable,P.S
Expressed Sequence Tags from B73 Maize Seedlings and Silks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR PRimers
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                                                                                                                                                                                    121
                                                                                                               Conservative
                                                                                                                                                                                  schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST29-D08"
                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
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                                                                                                                             37.0%;
98.0%;
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Pred. No. 7.2
                                                                                                                 Mismatches
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91.3%;

Pred. No.

6.8e-66;

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                                                                                                                                                                  Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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BG463106
BG463106.1
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The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA:
                                                                                                                                                                                                                                                        Contact: Cordonnier-Pratt MM
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Reid, S.P., Cordonnier-Pratt, M.-M.,
An EST database from Sorghum: deve
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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EM1_47_E12.b1_A002
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706 583 0210
     /clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
BCORI; The library was made from poly-A RNA in the cloning
vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."
a 219 c 192 g 90 t
                                                                                /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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Query Match

37.0%;

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                                                                                                   Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of P
Plant Sciences Building, Rm. 2502, Athens,
                is 20.
                                         Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been tri
                                                                                                                                                                                                           clade; Panicoideae; Andropogoneae;
1 (bases 1 to 593)
Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoidae; Andropogoneae; Sorghum.
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Sorghum bicolor
                              below Phred
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532; Conservative
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BE362356
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sorghum.
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 591)
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/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
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Query Match
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                                                        TGTCGCCCACGCACAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAG 179
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                                                                                                                   GCTGGGCCGGCGGACTCGACGACGGCGAGCGCGTCCCTTGCCAACAGCAACCTCCCGCA
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Sequences have been trimmed
below Phred quality 16. The
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Fax: 706 583 0210
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The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
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Unpublished (2000)
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s excision.!
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 CCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAG
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
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BE361528
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/db_xref="taxon:4558"
/clone="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 215 c 186 g 113 t
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cordonnier-Pratt MM
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                                                                                          Conservative
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/note="Organ: Embryos germinated for 24 hr; Vector: /note="Organ: Embryos germinated for 24 hr; Vector: /pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

214 c 190 g 87 t
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                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                     36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Sorghum:
                                                                                       Score 489.6; DB Pred. No. 3e-64; 0; Mismatches
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5 1
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(EM1)
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bicolor
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cDNA,
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mRNA
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RESULT 11
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                                                                                                                                                                                                                    An EST database from Sorghum: pathogen-induced plants Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Than Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                          is
Seq
                                                                                                                                                   Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PI1
                                                                                                                                                                                                                                                                                                                               clade; Panicoideae; Andropogoneae; Sorghum.
l (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                   sorghum.
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                               EST
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_69_D10.b1_A002 Pathogen :
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706 583 0210
                                                                                                            quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
/clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leave
two-week-old sorghum plants 48 hr after
                                          /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                 Location/Qualifiers
                                                                                                            stop:
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                                                                                                                                                      to exclude PolyA,
threshold for high
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1 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                                   highest quality
                  leaves
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                                                                                                                                                                 vector and regions
    inoculation;
                  from
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CGCTGTTCAGCAGGCAGGCCTGTCGGCGCGCGACA

589

sequence. BE361738 BE361738.1 EST.

<u>;</u>_

BE361738 DG1_82_H08.b1_A002

Dark

Grown

) _p

mRNA lin (DG1) Sorghum

near EST 20-JUL-2000 bicolor cDNA, mRNA

Sorghum

bicolor

sorghum

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Best Local
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                                                                                                   TTCAAGGCTGCGACGGATCGATCCTTCTCGACGCCGGAGGGGAGAAGACCGCCGGGCCGA 328
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CCCTGTTCGGCAGGCAGGGCCTGTCGCCGCGCGACA 604
                                                      GCGCCTCGCTCGCCAACAGCAACCCCCCGCCCCCGACGGCCAGCCTCGGCACGCTCATCT
                                                                                                                     CGTGCCCCGGCGTCGTCGTGCGCCGACATCCTTGCCCTTGCCGCGGCGAACCGAACCA
                                                                                                                                                                                                                                                          ACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAGGCCG
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                                  GCGCGTCCCTTGCCAACAGCAACCTCCCGCAGTCGACGGCGAGCCTGGGTACGCTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptibility to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: while most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; Two-week-old sorghum plants (ETX 623 cultivar) were infected with pathogen (isolate FRM42I of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 461.4; DB Pred. No. 5e-60;
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REFERENCE AUTHORS

COMMENT

TITLE JOURNAL

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Matches 476; Conserv
               CTGCAGAGCATCGTTCGGGCGGCGGCGATGACCCCAGGCCGTCGCAAGTGAGCAGAGGATGGGC
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                                                                                                                                             GAGGTCATCGACACCATCAAGACCAACGTGGAGGCCGCGTGCCCCGGCGTCGTGTCGTGC
                                                                                                                                                                                                                                                                                                CTTCTCGACGCCGGAGGGGAGAAGACGCCGCCGGCCCGAACCTGAACTCGGTGCGCGGCTTT 351
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                                                                                                                                                                             An EST database from Sorghum: dark-grown Seeully, An EST database from Sorghum: dark-grown Seeully, Dupublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nmpratt@uga.edu sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 561)
Crononnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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Seq primer: JEN REV
High quality sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/clone_Torgan: 5-day-old dark-grown seedlings; Vector:
/mote="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 195 c 166 g 106 t
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Pred. No. 3.6e
0; Mismatches
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es 56;
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                                                                                                                                                                                                                                                                                        TCATTCACCGAGCGTGCAGGCAGGCAGCAGCTTGCCCATGGCGTCTCCCCACCTTGATGC 88
                                                                                                             TTCAAGGCTGCGACGGATCGATCCTTCTCGACGCCGGAGGGGAAAGACCGCCGGGCCGA 328
                                                                                                                                                                               TCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGCTCAGGCTCTTCTTCCACGACTGCTTCG
                                                                                                                                                                                                                                           TCTATGCGTCCTCCTGCCCAACCTGCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCG 208
                                                                                                                                                                                                                                                                                                                                                          ACGCCAATTCGGCGCGCGCTTTGAGGTCATCGACACCATCAAGACCAACGTGGAGGCCG
                                               ACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACCATCAAGCGGAACGTCGAGGCCG
                                                                                              TCTATGCATCCTCCTGCCCCAACCTGCAGAGCATCGTGCGGAGGGCGATGATCCAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Cordonnier-Pratt MM
Contact: For Genemics and Bioinformatics
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
BE358471
BE358471.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
clade; Panicoideae; Andropogoneae; Sorghum.
I (bases 1 to 570)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE358471 570 | DG1_30_A01.b1_A002 Dark Grown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,L.H.
An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="bark Grown 1 (DG1)"
/clone_llb="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/notea Tap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 198 c 167 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .570
                                                                                                                                                                                                                                                                                                                                                                                                                                        32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 442; DB 10;
Pred. No. 4.1e-57;
0; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to exclude PolyA, vector and in threshold for highest quality
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n l (DG1) Sorghum bicolor cl
                                                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 570;
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aceae; PACC
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BG841858/c
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCTGTTCAGCAGG 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR PRIMERS
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 446)
01u,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
0n May 25, 2001 this sequence version replaced gi:14208180.
Contact: Pattick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
Zea mays
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BG841858
BG841858.2
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MEST27-D09.T3 ISUM4-TN Zea mays cDNA clone MEST27-D09 3', mRNA
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Agronomy, Iowa State University, Ames, IA 50011-1010,
515-294-0975
                                                                                    /tissue_type="Seedling and silk"
//lab_host="DHIDB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MEST27-D09"
/clone_lib="ISUM4-TN"
  32.5%;
Score 439.6; DB 12; Pred. No. 1.1e-56;
                      Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sorghum bicolor
                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
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BE600142
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500 CGACGGCCAGCGTCGCTCGCCAACAGCACCCCCGCCCCCGACGGCCAGCCTCGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 ACTGCTTCGTTCAAGGCTGCGACGGATCGATCCTTCTCGACGCCGGAGGGGAGAAGACCG
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                                                                                                                                                                                                                                                                                                                     An EST database from Sorghum: pathogen-induced plants (npublished (2000))
Contact: Cordonnier Pratt MM
Laboratory for Genomics and Bioinformatics
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukáryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 564)
Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE600142 564 bp mRNA linear EST 18-AUG-2000 PRIL_79_611.bl_A002 Pathogen induced 1 (PII) Sorghum bicolor cDNA,
                                                                                                                                                                  Seq primer: JEN REV
High quality sequence stop:
POLYA=No.
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Pathogen induced 1 (PII)"
/clone_lib="Pathogen induced 1 (PII)"
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inocula
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                ave been trimmed quality 16. The
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BASE COUNT
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                                                                                                                                                                                                                     269 TTCAAGGCTGCGACGGATCGATCCTTCTCGACGCCGGAGGGGAGGAGGACGCCCGGGCCGA.328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TCTATGCATCCTCCTGCCCCAACCTGCAGAGCATCGTGCGGAGGGCGATGATCCAGGCCC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 CCCTGTTC 576
                                                                                           497 GCGCGTCCCTTGCCAACAGCAACCTCCCGCAGTCGACGCGAGCCTGGGTACGCTCATCT 556
                                                                                                                                            509 GCGCCTCGCCCAACAGCAACCCCCCCCCCCCGACGCCCAGCCTCGGCACGCTCATCT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 TCGCAAGTGAGCAGAGGATGGGCGCCTCTCTGCTGCAGGCTCTTCTTCCACGACTGCTTCG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCTGTTC 564
                                                                                                                                                                                          ATCTGCTCGGCGGGCCGACCTGGAACGTGCCGCTGGGCCGGCGGACTCGACGACGCGA 496
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Search completed: May 3, 2003, 09:24:37 Job time: 1461 secs

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Match Length DB
     Published_Applications_NA: *
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Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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US-09-938-842A-1714

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US-09-938-842A-783

US-09-938-842A-783

US-09-938-842A-1718

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US-09-938-842A-173
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US-09-938-842A-1711
US-09-938-842A-1632
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sequence 11, Appl
sequence 2545, Appl
sequence 83, Appl
sequence 1711, Ap
sequence 1163, Ap
sequence 1167, Ap
sequence 2559, Ap
sequence 2693, Ap
sequence 1980, Ap
sequence 1714, Ap
sequence 783, Appl
sequence 783, Appl
sequence 1518, Ap
sequence 1719, Ap
sequence 1773, Appl
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262 954 1116	990 990 1181 1074	1062 972 303	1062 1062	966 1041 1062	318 285 239	1014 969 373 441	1045 235 978
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Sequence 2630, Ap Sequence 2570, Ap Sequence 2181, Ap	Sequence 20, Ap Sequence 50, Appl Sequence 2656, Ap	Sequence 3, App11 Sequence 682, App Sequence 3718, Ap Sequence 1506 An	Sequence 3, Appli Sequence 3, Appli	Sequence 1498, Ap Sequence 858, App Sequence 1457, Ap	Sequence 3642, Ap Sequence 8092, Ap Sequence 2727, Ap	Sequence 21, App Sequence 2446, App Sequence 710, App Sequence 907, App	Sequence 166, App Sequence 97, Appl Sequence 2329, Ap

ALIGNMENTS

US-09-938-842A-60

Sequence 60, Application US/09938842A Patent No. US20020160378A1

GENERAL INFORMATION:

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Best Local Similarity 52.2%;
Matches 485; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
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APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1017
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                              174 GCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGCGC 233
                                                                                                                                                                                                   114 CTCCTGTGTCGCCCACGCACAGCTCTCGCCCCACGTTCTATGCGTCCTCCTGCCCCAACCT 173
                                       144 CGAGGAGATCGTGAGGTCAGTTGTAGCCAAAGCTGTTGCAAGGGAGACTCGTATGGCTGC
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TTCTCTCATGAGGCTCCATTTCCACGATTGTTTCGTTCAGGGTTGTGATGGATCGTTGCT
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109.8 107.4 105.4 103.4

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APPLICANT: Simmons, Carl
TITLE OF INVENTION: Maize Defense-Inducible Ge:
TITLE OF INVENTION: Use
FILE REFERENCE: 035718/239835
CURRENT APPLICATION NUMBER: US/10/027,559
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/243,120
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                     US-10-027-559-11
                                                                                                                                                                                                                                    Sequence 11, Application US/10027559 Patent No. US20020144307A1 GENERAL INFORMATION:
                                                     SOFTWARE: FastSEQ for SEQ ID NO 11
      LENGTH: 12
TYPE: DNA
ORGANISM:
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                                                                                                AACGCAACCATGAAGGCGCTGGTCGACTCCTTCGTGCGCAGGCGAGGCCACGTGGAAGACC
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CAGATCAGGCGCAACTGCCGGGTCGTCAAC
                                AAGTTCGCCAAGTCCATGCTCAAGATGGGGGCAGATCGAGGTGCTCACGGGGACGCAGGGC
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                                                                                                                                                                 TACTACGTCGGCCTCACCAACAACCTGGGCCTCTTCGAGTCGGACGCGGCGCTGCTGACC
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                                                                                                                                                                                                                                                                                                                                                                                               CGCATCTACGGCGACACCGACATCAACGCCT-------
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Peroxidase-like
; NAME/KEY: CDS
; LOCATION: (18)...(1088)
US-10-027-559-11
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.8
Matches 491; Conservative
                                                                                                                                                                                            136 CTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAGAGCATCGTTCGGGCGGCG
                                                            144 GTGGCCGCCGCGTTCACCAACAACTCCGGCGTCGCTCCGGCGCTCCTCCGCATGCACTTC
                                                                                                                                                  84 CTCGAGTTCGGTTTCTACAACAAGACGTGCCCCAGCGCCGAGACCATCGTGCAGCAGACC
CACGACTGCTTCGTTCAAGGCTGCGACGGATCGATCCTTCTCGACGCCGGAGGGGAGAAG
                                                                                      ATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGGCGCCTCTCTGCTCAGGCTCTTCTTC 255
                                                                                                                                                                                                                                                           12.7%;
                                                                                                                                                                                                                                      Score 172.4; DB 12;
Pred. No. 2.2e-36;
0; Mismatches 376;
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US-09-938-842A-2545; Sequence 2545, Application; Patent No. US20020160378A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1011
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 CCTGTGTCGCCCACGCACACGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCCAACCTGC
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                                                                                                                                                                                   AGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGCGCCT
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               GGTGCACCATCCGCGGCGGCCATCTACGGCGACACCGACA:
                                                                        AGGGCCTGTCGCCGCGCGACATGACGGCGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCC 643
                                                                                                                                ACAGCAACCCCCCGCCCCGACGGCCAGCCTCGGCACGCTCATCTCCCTGTTCGGCAGGC
                                                                                                                                                             CGAGCTGGGAAGTACCTCTAGGAAGAAGAAGACGCGAGGAGGAGCAAGCTTGAGTGGTTCCA
                                                                                                                                                                                                                     TTTCTTGCGCTGATATCTTGGCTCTAGCCGCTAGAGACTCAACTGTTATTACGGGTGGAC
                                                                                                                                                                                                                                                  GTGGTTTCGAACTCATCGAGGAAATCAAACATGCCTTAGAACAAGAGTGTCCTGAAACAG
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                                                                                                                                                                                                                                                                                                                                         TGGACAGCAGTGGAACCATAATCAGCGAGAAACGATCAAACCCTAACAGAAACTCAGCCC
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                                            AAGGCCTTGATCTCGTCGATCTTGTCTCCCTCTCAGGAAGTCACACCATTGGAAACTCGA
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Pred. No. 3.
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3.6e-36;
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US-09-894-633A-83
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SEQ ID NO 83
LENGTH: 824
TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 425; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020124285A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 83, Application US/09894633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/894,633A CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/894,633 PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MASUCCI, JAMES
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPREFILE REFERENCE: 38-21(15856)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/214,357
PRIOR FILING DATE: 2000-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Conner, Timothy
                                                 187
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                                                                                                                                                                                                                                                                                  172 CTGCAGAGCATCGTTCGGGCGGCGATGACCCAGGCCGTCGCAAGTGAGCAGAGGATGGGC 231
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TCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACGTCGAGGCCGCGTGCCCC 396
                                                 CTGATCGCGTCCACCCAGTTCCAGAAGTCGGAGCACGACGCGGAGATCAACCACTCCCTC 246
                                                                                             CTTCTCGACGCCGGAGGGGAGAAGACCGCCGGGCCGAACCTGAA----
                                                                                                                                                                                      CTGGCGGGCGGCGGCGGCGCCCTGAAGCCGGACTTCTATAGCCAGTCGTGCCCGCGC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGCAGCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGCCGGACAGATCA 979
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                                                                                                                                            GCGGGCCTGCTCCGCGTCTTCTTCCACGACTGCTTCGTCAGCGGGTGCGACGCGTCGGTG 186
                                                                                                                                                                                                                                     GCGGAGCGGATCATTGCGGAGGTGATGCAGACGAAGCAGATGGCGAACCCGACGACGGCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGTATCTGTCGGAGGGTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTCCAAGGAGCTGGGAGCTATACGCTGAGAATCAAGAGGCCTTCTTTGAGCAGTTTG
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54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PRIOR PRIOR NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1711
PRIOR FILING DATE: 2001-06-22
LENGTH: 996
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; Sequence 1711, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
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                                                                                                               ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1711
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                                                                 Query Match
Best Local
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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                                                                 Similarity
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                                                              11.1%;
                                               0;
                                             Score 150; DB 9; Lo
Pred. No. 2e-30;
0; Mismatches 435;
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Sequence 1632, Application Patent No. US20020160378A1 GENERAL INFORMATION:
APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel

US/09938842A

APPLICANT:
APPLICANT:
TITLE OF IN

T: Wang, Xun
T: Zhu, Tong
INVENTION: STRESS-REGULATED GENES

OF

PLANTS,

TRANSGENIC PLANTS CONTAINING

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FITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1632
LENGTH: 1041
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Best Local Similarity 50.7%;
Matches 448; Conservative
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                                                                                                     CAGACGCCGGTGAGGTTCGACACGGCCTACTTCACCAACCTGCTGTCGCGGCGGGGGCCTG 825
                                                                                                                                                             TTCCGCGGCCGCATCTACGGCGACACCGACATCAACGCCTCCTTCGCGGCGCCTGCGGCAG 714
                                                                                                                                                                                                                                                                                                            AGAGAAGCTGTCGTCCTCACTGGAGGACCGTTTTGGCCCGTGCCTTTGGGACGAAGGGAC
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TTGGATTCTGATCAAACCCTAATGACAGATCCTACGGCTGCCGCCTTGGTGAAGTCGTAC
                                   TTCCACTCGGACCAGGAGCTCTTCAACGGCGGGTCGCAGGACGCGCTGGTGAGGCAGTAC 885
                                                                     GCTAGCTCAGTCAAGTTTGACAATGCTTACTACGTGAACTTAATGAACAACATAGGACTG
                                                                                                                                           CTAAAGGACACGTGTCCTAACGTGGACTCCTCAGACTCTAAGCTCGCTGCTCTTGACGCA 801
                                                                                                                                                                                                                TTCAAGGGCTCAGGCCAGCCTGACCCAAACCTAGCCGCTTCCTCAGCACTTCTCTCTAAG
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Pred. No. 1.3e-27;
0; Mismatches 394; Indels 42;
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PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 1167
LENGTH: 251
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700158231H1
US-09-923-876-1167
                                                                                                                                                                                              US-09-938-842A-2559
                                                                                                                                                                                                                    RESULT 8
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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Dhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                          Sequence 2559, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.3
Matches 180; Conservative
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
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CURRENT FILING DATE: 2001-08-06
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Pred. No. 7.8e-25;
0; Mismatches 68;
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                                        TRANSGENIC PLANTS CONTAINING
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CURRENT APPLICATION NUMBER: US/09/938.842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2559
LENGTH: 1011
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2559
               PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 3446
LENGTH: 234
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US-09-923-876-3446, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:
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                                                                                                                                                                                       APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
FILE REFERENCE: PL-0012-1 COM
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
CURRENT FILING DATE: 2001-08-06
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 TCCGAATGTCCTGGAGTTGTTTCATGCGCTGATCTTCTCACAATTGGTGCTAGAGATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACACCATCGGGCAGGCCGGGTGCACCACCTTCCGCGGCCGCATCTACGGCGA 677
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700162281H1
US-09-923-876-3446
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                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Arabidopsis thaliana; US-09-938-842A-2693
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APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2693
LENGTH: 993
                                                                                                                                                                                                                                                                                                              Matches 439;
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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APPLICANT: Kreps, Joel
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ATGAAGACGCAGAAAGACGCAGATGACAATAAATCTCTCGCCGGAGACGGATTTGACA 325
                                      --GACGCCGGAGGGGAGAAGACCGCCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGG 355
                                                                               TGTTCTTTCACGACTGCTTCGTCGAGGGATGTGATGCGTCTGTGTTTATAGCATCTGAGA 265
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 Mismatches

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Pred. No. 1.4
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APPLICANT: Harper, Jeff
APPLICANT: Wang, Yoel
APPLICANT: Wang, Yoel
APPLICANT: Wang, You
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,547
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
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NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1980
LENGTH: 1077
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                            CGGGTCGTCAACAGCTAGATACGACGCATCGGA 1023
                                                                        ATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGCCGGACAGATCAGGCGCAACTGC 990
                                                                                                                                           CTGGTGAGGCAGTACAGCGCCAGCGCCTCGCTCTTCAACGCCGACTTCGTGGCAGCCATG
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                                                         ATCAAGATGGGGAACATTAGTCCCTTGACTGGGAGTAGTGGAGAGATTAGACAAGACTGT
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51; Conservative
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48.3%; Pred. No. 2.7e-21
rative 0; Mismatches 44
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRITTLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIEJ300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1714
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US-09-938-842A-1714
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Best Local Similarity 48.1%;
Matches 455; Conservative
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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GCCGCATCTACGGCGACACCGACATCAACGCCTCCTTCGCGGCGCTGCGGCAGCAGACGT
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                                                 CGCATACGTTCGGGCGTGCTCGATGTGGAGTATTCAACAACAGACTATTTAACTTCAGCG
                                                                               CGCACACCATCGGGCAGGCCCGGTG-----
                                                                                                               TCACATTTAAATTTTCGGCTGTCGGGCTTAATACAAACGATCTGGTAGCCTTATCTGGTG
                                                                                                                                               CGGCCAACCTCGCCGGTGCAAATTCGTCCATTCCTTCTCCCATCGAAAGCCTAAGCAACA 532
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                                                                                 -CACCACCTTCCGCG 661
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIF1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3367
LENGTH: 942
TYPE: DNA
GRGANISM: Arabidopsis thaliana
US-09-938-842A-2367
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US-09-938-842A-2367
Sequence 2367, Application US/09938842A
Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 437
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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les 437; Conserv
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CTGCTGGACCAAACGGAAGCGTCAGGGAATTTGACCTGATAGACCGGATCAAGGCTCAGC
                                                CCGGGCCGAACCTGAACTCGGTGCGCGGCTTTGAGGTCATCGACACCATCAAGCGGAACG
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46.9%; Pred. No. 9.8e-21;
ative 0; Mismatches 480
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CURRENT FILING DATE: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 783
LENGTH: 981
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US-09-938-842A-783
; Sequence 783, Ap
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
TYPE: DNA ORGANISM: Arabidopsis thaliana -09-938-842A-783
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1518
LENGTH: 987
                                   '; TYPE: DNA; ORGANISM: Arabidopsis thaliana US-09-938-842A-1518
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Best Local Sim
Matches 286;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1518, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
 Query Match
                                                                                                                                                                                                                                                APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE REFERENCE: SCRIPJ300-3
CURRENT FILL REFERENCE: SCRIPJ300-3
CURRENT FILING DATE: 2001-08-24
CURRENT FILING DATE: 2001-08-24
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Pred. No. 1.4e-20;
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                                                                                                                                                                                                                                                                        648 ACAAACCGCAGATCCAACCATCGACCCAACATTTTTGGCGCAGCTTCAAACACAATGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 AGCCGCGTGTCCTGGAGTTGTCTCTTGTGCTGATATTTTAGCATTAGCCGCTCGTGACAC 410
                                                                                                                                                               768 CACTTCTTACTACAACAACCTAAGCCGTGGGCGTGGAGTTCTCCAATCCGATCAAGTCCT
                                                                                                                                                                                                                CCAAAACGGCGACGGTTCAGTGCGCGTGGATCTCGACACCGGAAGCGGAAGCACTTGGGA
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Search completed: May 3, 2003, 10:14:37 Job time: 137 secs

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      Pred. No. is the number of results predicted by chance to have a
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

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US-08-671-320-11

US-08-671-320-11

US-08-686-577-13

US-08-686-577-15

US-08-665-577-15

US-08-671-320-17

US-08-671-320-17

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ALIGNMENTS

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Best Local
                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEC ID NOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
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TSITFDNKYYSNLKIQKGLLHSDQQLFNGGSTDSQVTAYSSNQNSFFIDFTAAMVKMGNI
                     TPVREDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNV 294
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                                                                                                                                                                                                                                                                                                                                                                                 Score 965; DB 4;
Pred. No. 2.4e-95;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Length 318;
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295 GVLTGTAGQIRRNCRVVN 312

SPLTGTNGQIRKNCRKSN 318

US-09-615-192A-395

GENERAL INFORMATION:

Patent No. 64107

Sequence 395, Application US/09615192A

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RESULT 3
US-09-615-192A-378
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                             GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, IIkka
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION: Modification of Plant
FILE REFERENCE: 11000.1003c4U
                                                                                                                                                       Sequence 378, Application US/09615192A Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FOR SEQ ID NO 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1999-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
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                                                                                                                                                                                                                                                                     310 GTSGQIPKNCRKPN 323
                                                                                                                                                                                                                                                                                                 299 GTAGQIRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                           250 FDKNYYSDLKSQKGLLHSDQELFNGGSTDSQVTTYASNQNTFFSDFAAAMVKMGNIKPLT
                                                                                                                                                                                                                                                                                                                                                               239 FDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLT 298
                                                                                                                                                                                                                                                                                                                                                                                                                     190 VALSGGHTIGQAQCKNFRAHIYNETNIDSAYATSLRSKCPSTTGSGDSNLSPLDYMTPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRS--GGDGNLAPIDVQTPVR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 IAARDSVVELGGPSWTVMLGRRDSTTASKSGANSNIPPPTSSLSNLISLFQAQGLSAKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CIAVMVFIVCSITDTVNGQLSSTFYDKSCPTALSVVKAAVKQAVANEKRMGASLLRLHFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 CLVAVSLLSC----VAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRUGASLLRLFFH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 3.0
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                                                     Lignin
                                                                       for the
                                                       Content
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1 MASPTLMQCLVAVSLLSC--VAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASL 58

Matches 170;

Conservative

32;

58;

Indels

6;

Gaps

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; ORGANISM: Pinus radiata US-09-615-192A-394
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                                                                                                                                                                          PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 394
                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bloksberg,
APPLICANT: Havukkala,
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LENGTH: 315
                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
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PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
                                                                                                                                                        LENGTH: 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 VKNMVALSGSHTIGLARCTSFRRIYNDSNIDTSFAHKLQKICPRIGNDSVLQRLDIQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 PRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 DILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGRQGLS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 TFFDNLYYHNLLQKKGLLHSDQELFNGSSVDSLVKKYACDTGKFFRDFAKAMIKMSEIKP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 VRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 DIVALAARDSVVHLGGPSWTVSLGRKDSITASRSLANTSIPPPTSNLSALITSFAAQGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LFFHDCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 56.1%; Score 899.5; DB of Cocal Similarity 57.0%; Pred. No. 2.5e-88; es 180; Conservative 46; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVGFSVVVVLLATSVIT-TARCKLSPSHYQSTCPKALSIVRAGVAKAIKNETRTGASLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bloksberg, Leonard N.
                                                                                                                                                                                                   for Windows Version 3.
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                      52.7%;
63.9%;
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Score 846; DB 4;
Pred. No. 1.1e-82;
2; Mismatches 58
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                                        Length 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2,
Patent No.
                                                                Matches
                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEPAX: 317 337 4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMA
                                                                                                                                                                                   TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                            TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WOOSley TITLE OF INVENTION:
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                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>بـــ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | MASFTAMRSLAFIALLMCSTVAYAQLSATFYNTSCPKLLSTVQAAVKQAVANEKRMGASL 60
                  TLMQCLVAVSLLSCVAHAQ------LSPTFYASSCPNLQSIVRAAMTQAVASEQRMGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSPRDMTALSGAHTIGOARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQG
TSMGCLVLLCLVSSLLPSAVLGHPWGGLFPQFYDHSCPKAKEIVQSIVAQAVAKETRMAA: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSTKDMVVLSGAHTIGQARCTSFRARIYNESNINAAYATSLKTNCPTTGSDNNLSPLDRV 24(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2, Application US/09097319A
3. 6384207
                                                                              Similarity
                                                                                                                                                           amino acid
)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woosley, Aaron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Folkerts, Otto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, Kelley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petolino,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pareddy, Dayakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Menke, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hopkins, Nicole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Belmar, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ainley, Michael
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                                                             51.2%; Score 822; DB 4;
51.1%; Pred. No. 5.8e-80;
tive 51; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Joseph F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katherine
                                                                                                                                                                                                                                                                                                                                                       US/09/097,319A
                                                                                            Length 333;
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APPLICANT: Bloksbery, APPLICANT: Havukkala, Ilka
FITLE OF INVENTION: Materials and Methods for TITLE OF INVENTION: Modification of Plant Lig FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
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SEQ ID NO 387
LENGTH: 287
TYPE: PRT
ORGANISM: Pinus radiata
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Best Local Similarity
Matches 162; Conserv
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CORTWARE: FastSEQ for Windows Version 3.
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246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 GNLAPIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQD-ALVRQYSASASLFNADF 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
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                                                                                                                                                                                                                                                                                                                                                        6 CIAVIVFIICSITDTVNGKLSSTFYDKSCPKALSIVQAGVKQAVAKEKRMGASLLRLHFH 65
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                                                                                                                                                                                                                                                                                         DCFVQGCDGSILLDAG----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILA 120
FDKNYYYNLKSKRGLLHSDQELFNGGSTDSHVTKYASNQNTF 287
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                                      FDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLF 280
                                                                                   VALSGGHTIGQAQCKNFRAHIYNDTNIDTTYATSLRSKCPSTTGSGDSNLSPLDYTTPTV 245
                                                                                                                                                                            IAARDSVVQLGGPSWKVMLGRRDSTTASISGANNNIPPPTSNLTKLISLFQAQGLSTKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                              50.3%; score 807; DB 4; 57.4%; Pred. No. 1.9e-78; tive 35; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-615-192A-397
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 397, Application US/09615192A Patent No. 6410718
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                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 397
LENGTH: 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. 6278041el Peroxidase Gene Sequences FILE REFERENCE: S-31081P1 CURRENT APPLICATION NUMBER: US/09/365,150 CURRENT FILING DATE: 1999-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lagrimini, Ma
APPLICANT: Desai, Nalini
ORGANISM: Pinus radiata -09-615-192A-397
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                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08//13,000
PRIOR EILING DATE: 196-09-11
PRIOR FILING DATE: US 09/169,789
                                                                                                                                             PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                              FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Tikka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of plant Lignin Content
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDTAYFTNLLSRRGLFHSDQELF--NGGSQDALVRQYSASASLFNADFVAAMIRMGNVGV 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDNDYFTNLQNNQGLLQTDQELFSTSGSATIAIVNRYAGSQTQFFDDFVSSMIKLGNISP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt HTFGRARCGTFEQRLFNFSGSGNPDPTVDATFLQTLQGICPQGGNNGNTFTNLDISTPND}
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Pred. No. 1.9e-68;
"""matches 97;
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Best Local Similarity
Matches 142; Conserv
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SEQ ID NO 391
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Best Local Similarity 64.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Materials and Methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 VN 312
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                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTLFTSDQTLYTDTRTRDIVINFAVNQSLFFEQFVLSMLKMGQLDVLTGSEGEIRKNCWA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRLYNSTTGTQMRDPTMDQSFAKNLYLTCPTS-TTVNTTKLDIRTPNVFDNKYYVDLLNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRRDSLTFANRSTYLANLPSPTSNYTGLISVLGPKGLNFTDLVALSGGHTIGRSNCSSFD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRRDSTT-ASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAHTIGQARCTTFR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEQTAPPNLSLRAQALKIINDIKENVEAACSGIVSCADIVTLAARDSVVMAGGPFYPLPL 150
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                                                                                                                     CADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQG 174
                                                                                                                                                                                 LRLHFHDCFVNGCDGSVLLDDSSSLTGEKTALPNNNSLRGFDVIDTIKSQVEAVCSGIVS
                                                                                                                                                                                                                        LRLFFHDCFVQGCDGSTLLDAG-----GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVS 114
LSPRDMTALSGAHTIGQARCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1997-11-21
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BER: US 08/975,316
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47.0%; Pred. No. 5.7e-63;
tive 55; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ilkka
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Pred. No. 4.8e-59;
1; Mismatches 44
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US-08-671-320-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: 1125 SO. 103RD STREET
STREET: SUITE 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                  292 GNVGVLTGTAGQIRRNCRVVNS 313
                                                                                                                                                   184 LSGAHTIGIAHCSSLSNRLFNFTGKGDQDPSLDSEYAANLKAFKC-TDLNKLNTTKIEMD 242
                                                                                                                                                                                     183 LSGAHTIGQARCTTFRGRIY-----GDTD--INASFAA-LRQQTCPRSGGDGNLAPIDVQ 234
                                                                                                                                                                                                                                                               123 ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182
303 GRINVKTGTEGEIRKHCAFLNS 324
                                                                                                                                                                                                                            124 ARDTIVATGGPFWKVPTGRRDGVISNLTEARDNIPAPSSNFTTLQTLFANQGLDLKDLVL 183
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: OMAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                    6 LMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHD 65
                                                                                                                                                                                                                                                                                                                                                                                  8 LSLCLLA----LIASTHAQLQLGFYAKSCPNAEQIVLKFVHDHIHNAPSLAAALIRMHFHD 64
                                                                         PGSRKTFDLSYYSHVIKRRGLFESDAALLTNSVTKAQIIELLEGSVENFFAEFATSMEKM 302
                                                                                                            TPVR--FDTAYFTNLLSRRGLFHSDQELF-NGGSQDALVRQYSASASLFNADFVAAMIRM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68124-1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402-398-9005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.7%; Score 605.5; DB 2
42.5%; Pred. No. 9.7e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/671,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 19;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-868-577-13
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Vierli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 402-333-1510 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acid
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                                                                                                                                                          183 LSGAHTIGQARCTTERGRIY-----GDTD--INASFAA-LRQQTCPRSGGDGNLAPIDVQ 234
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303 GRINVKTGTEGEIRKHCAFLNS 324
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                  66 CFVQGCDGSILLDA---GGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                    6 LMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHD 65
                                                                                                                                                                                                                               ARDGTNILGGPTWSVPLGRRDSTTASASLANSNPPPPPTASLGTLISLFGRQGLSPRDMTA 182
                                                                                                                                                                                                                                                                                GNVGVLTGTAGQIRRNCRVVNS 313
                                                                   PGSRKTFDLSYYSHVIKRRGLFESDAALLTNSVTKAQIIELLEGSVENFFAEFATSMEKM 302
                                                                                                                                                                                                           ARDTIVATGGPFWKVPTGRRDGVISNLTEARDNIPAPSSNFTTLQTLFANQGLDLKDLVL 183
                                                                                                                                                                                                                                                                                                                                                    LSLCLLA---LIASTHAQLQLGFYAKSCPNAEQIVLKFVHDHIHNAPSLAAALIRMHFHD
                                                                                                   TPVR--FDTAYFTNLLSRRGLFHSDQELF-NGGSQDALVRQYSASASLFNADFVAAMIRM 291
                                                                                                                                         LSGAHTIGIAHCSSLSNRLFNFTGKGDQDPSLDSEYAANLKAFKC-TDLNKLNTTKIEMD
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555 13th Street NW, Suite 701 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 amino acids
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 9.7e-57;
4; Mismatches 112;
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RESULT 12 US-08-671-320-11 ; Sequence 11, Application US/08671320 ; Patent No. 5840558

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                                                                                                                       RESULT 13
US-08-868-577-11
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Best Local (
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                                                                                      Patent No. 5866695
                                                                                                       Sequence 11,
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INFORMATION FOR SEQ ID NO: 11:
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Patent NO. JOYAN AND PARENTI NI PROPERTION:
GENERAL INFORMATION:
APPLICANT: Vierling Jr., Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: 1125 SO. 103RD STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 CFVRGCDASYLLNSTINQAEKNAPPNL-TVRGFDFIDRIKSLVEAECPGVVSCADILTLA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 CFVQGCDGSILLDA---GGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/671,320
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                                                                                                                                                                                                                                                       PGSRKTFDLSYYSHVIKRRGLFESDAALLTNSVTKAQIIQLLEGSVENFFAEFATSIEKM
                                                                                                                                                                                                                                                                                      TPVR--FDTAYFTNLLSRRGLFHSDQELF-NGGSQDALVRQYSASASLFNADFVAAMIRM 291
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                                                                                                                                                                                       GRINVKTGTEGEIRKHCAFINS
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Similarity 42.2%;
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                                                                                                     Application US/08868577
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Pred. No. 1.2e-56;
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                           PEROXIDASE
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                           ACTIVITY
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; MOLECULE TYPE: protein US-08-868-577-11
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                                                                                                                                                       Sequence 10, Application US/08190029A Patent No. 5736363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                         GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Jondle, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
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  NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF,
STREET: 10 S. WACKER DRIVE, SUIT
                                                                   APPLICANT: EDWARDS, KICHALL APPLICANT: BAWDEN, Lindsey TITLE OF INVENTION: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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STREET:
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555 13th Street NW, Suite 701 East
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                                                                                                                      EDWARDS, Richard Mark
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                                                                               IGF-II ANALOGUES
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      SUITE
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CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A
ZID.

U.S.A. 60606 R PT

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RESULF 15
US-08-462-695-10
US-08-62-695-10
; Sequence 10, Application US/08462695
; Patent No. 5854025
; GENERAL INFORMATION:
: GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 349 amino acids

TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear
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36.5%; Score 585.5; DB 1; Length 349;
Best Local Similarity 45.6%; Pred. No. 1.5e-54;
Matches 128; Conservative 34; Mismatches 104; Indels 15;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/08/190,029A
FILING DATE: 28-FEB-1994
CLASSIFICATION NUMBER: PCT/GB92/01389
FILING DATE: 27-UUL-1992
PRIOR APPLICATION NUMBER: GB 9202401.7
PILING DATE: 05-FEB-1992
PRIOR APPLICATION MUMBER: GB 9116325.3
PRIOR APPLICATION NUMBER: GB 9116325.3
PRIOR APPLICATION NUMBER: GB 9116325.3
PRIOR APPLICATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 94,662
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STREAMSTON:
TELECOMMUNICATION STREAMSTON:
TELECOMMUNICATION NUMBER: 94,662
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                                                                    APPLICANT: EDWARDS, Richard Mark
APPLICANT: BAWDEN, Lindsey
TITLE OF INVENTION: IGF-II ANALOGUES
                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 FRTEKDAFGNANSARGFPVIDRMKAAVESACPRTVSCADLLTIAAQQSVTLAGGPSWRVP 121
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   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QLTPTFYDNSCPNVSNIVRDTIVNELRSDPRIAASILRLHFHDCFVNGCDASILLDNTTS 61
                                                                                                                                                                                                                                                                                                                                                                                                RGLFHSDQELF---NGGSQDALVRQYSASASLFNADFVAAM 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWSVP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDRLYNFSNTGLPDPTLNTTYLQTLRGLCPLNGNLSALVDFDLRTPTIFDNKYYVNLEEQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGRIYG-----DIDINASFAALROOTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSR 250
BANNER & ALLEGRETTI, LTD
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TELEPAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-695-10
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Search completed: April 26, 2003, 12:36:14 Job time: 31 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/462,695
FILING DATE: 5-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/190,029
FILING DATE: 28-FEB-1994
PRIOR APPLICATION NUMBER: PCT/GB92/01389
FILING DATE: 27-UUL-1992
PRIOR APPLICATION NUMBER: B 9202401.7
APPLICATION NUMBER: GB 9202401.7
FILING DATE: 05-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9116325.3
FILING DATE: 09-VUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J MCDONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 312-715-1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: LLL.
COUNTRY: U.S
OTP: 60606
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OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                          242
                                                                                                                                                                                                                            198
                                                                                                                                                                                182 MDRLYNFSNTGLPDPTLNTTYLQTLRGLCPLNGNLSALVDFDLRTPTIFDNKYYVNLEEQ 241
                                                                                                                                                                                                                                                                      122 LGRRDSLQAFLDLANANLPAPFFTLPQLKDSFRNVGLNRSSDLVALSGGHTFGKNQCRFI 181
                                                                                                                                                                                                                                                                                                             139 LGRRDSTTASASLANSNPPPPTASLGTLISLEGRQGLS-PRDMTALSGAHTIGQARCTTF 197
                                                                                                                                 251 RGLFHSDQELF---NGGSQDALVRQYSASASLFNADFVAAM 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 10 S. WACKER DRIVE, CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FRIEKDAFGNANSARGEPVIDRMKAAVESACPRIVSCADLLTIAAQQSVTLAGGPSWRVP 121
                                                                                                                                                                                                                                                                                                                                                                                                        79 AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWSVP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QLTPTEYDNSCPNVSNIVRDTIVNELRSDPRIAASILRLHFHDCFVNGCDASILLDNTTS 61
                                                                                                                                                                                                                          RGRIYG-----DTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSR 250
                                                                                          KGLIQSDQELFSSPNATDTIPLVRSFANSTQTFFNAFVEAM
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Y: U.S.A.
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SYSTEM: PC-DOS/MS-DOS
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
    120
112
104.5
89.5
89.5
84.5
84.5
83.5
81.5
81.5
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132.5
126.5
125.5
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seq length: 2000000000
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1604
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_RUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_NEW.PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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13 US-10-027-559-6
10 US-09-870-501-1
10 US-09-885-329-6
10 US-09-885-329-6
10 US-09-885-329-2
10 US-09-885-329-2
10 US-09-885-329-2
10 US-09-885-329-4
10 US-09-981-9008-12
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Sequence 12, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 54, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 1802, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 205, App
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Simmons, Carl
TITLE OF INVENTION: Maize Defense-Inducible Genes and
TITLE OF INVENTION: Maize Defense-Inducible Genes and
TITLE OF INVENTION: Use
FILE REFERENCE: 035718/239835
CURRENT APPLICATION NUMBER: US/10/027,559
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/243,120
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 357
TYPE: PAT
ORGANISM: Zea mays
US-10-027-559-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application U Patent No. US20020144307A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-10-027-559-12
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Sequence 167, App	9 US-09-712-363-167	728	4.7	75.5	4 5
Sequence 10094, 1	10 US-09-815-242-10094		4.7	75.5	44
Sequence 5, Appli	9 US-10-014-717-5	7257	4.7	76	43
	9 US-10-101-464A-893		4.7	76	42
Sequence 48, App.	10 US-09-829-549A-48		4.7	76	41
~			4.8	76.5	40
128,		491	4.8	76.5	39
69, 1			4.8	76.5	3 8
Sequence 5860, Ap	9 US-09-738-626-5860	442	4.8	76.5	37
Sequence 11950, 2	10 US-09-815-242-11950			77	36
Sequence 10, Appl	9 US-10-092-880-10	1600		77.5	3 5
Sequence 9, Appli	9 US-10-092-880-9	1599		77.5	34
	10 US-09-749-728B-23	215			ω
Sequence 2, Appli	9 US-09-758-828-2	1334		78	32
Sequence 892, App				78	3 1
Sequence 6, Appli	9 US-09-976-059-6			78	30
Sequence 934, App	9 US-10-101-464A-934			78.5	29
Sequence 10446, A	10 US-09-815-242-10446			78.5	28
Sequence 38, Appl	9 US-09-928-457-38			79	27
Sequence 405, App	9 US-09-975-719-405			79	26
Sequence 11836, F			. 9	79	25
Sequence 6, Appli	9 US-10-192-584-6			79.5	24
Sequence 6011, Ap	9 US-09-738-626-6011	314 9	5.0	80	23
Sequence 5110, Ap	Sn			80	22
Sequence 2, Appli	10 US-09-782-906-2	39		80.5	21
Sequence 7, Appli	10 US-09-379-931-7	1026	5.1	81.5	20

ALIGNMENTS

Application US/10027559

and

Their

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Qy	Qy Db	Qy Db	Qy	Qу	Que Bes Mat
226 GNLAPIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFV 285	183 LSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGD 225	123 ARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTA 182	67 FVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALA 122 : : : : : : : : : : : : : : : :	9 CLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDC 66	Query Match 38.8%; Score 622.5; DB 12; Length 357; Best Local Similarity 40.4%; Pred. No. 1.8e-52; Matches 132; Conservative 56; Mismatches 116; Indeks 23; Gaps
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55;

Gaps

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; TYPE: PRT
; ORGANISM: Zea mays
US-10-027-559-6
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US-10-027-559-6
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-870-501-1
                                                                                           GENERAL INFORMATION:

APPLICANT: Takabe, Tetsuko
TITLE OF INVENTION: Persylsomal Ascorbate Peroxidase Gene Induced by High
TITLE OF INVENTION: Temperature Stress and a Trangeneic Plant Exhibiting
TITLE OF INVENTION: Thermotolerance
FILE REFERENCE: 026350-053
CURRENT APPLICATION NUMBER: US/09/870,501
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: JP 2000-172850
PRIOR REPLICATION NUMBER: JP 2000-172850
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10027559
Patent No. US20020144307A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl
TITLE OF INVENTION: Maize Defense-Inducible Genes and Their
TITLE OF INVENTION: Use
FILE REFERENCE: 035718/239835
CURRENT APPLICATION NUMBER: US/10/027,559
CURRENT APPLICATION NUMBER: 0001-10-23
PRIOR APPLICATION NUMBER: 60/243,120
PRIOR FILING DATE: 2000-10-25
NUMBER: GENERAL STATES AND APPLICATION NUMBER: 160/243,120
PRIOR FILING DATE: 2000-10-25
                           SOFTWARE: PatentIn
SEQ ID NO 1
LENGTH: 291
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09870501 Patent No. US20020100081A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 ALLSDPVFRPLVEKYAADEKAFFDDYKEAHLKLSELG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 ELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 SLANSNPPP----PTASLGT--LISLEGRQ-GLSPRDMTALSGAHTIGQARCTTFRGRIY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 KSMLKMGQIEVLTGTQGEIRRNCRVIN 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 ---KPQPPPEGRLPDATKGSDHLRQVFGKQMGLSHQDIVALSGGHTLG--RCHK----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·46 QAVASEQRMGASLLRLFFHDCFVQGCDGSILLDAG----GEKTAGP------NL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 NSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 RALIAEKSCAPLMLRLAWH-------SAGTFDVSSRTGGPFGTMKHQSELAHGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLS--RRGLFH--SDQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NA--GLDIAVRLLEPIKEEFP-ILSYADFYQLAGVVAVEVTGGPEIPFHPGRED-----
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US-09-870-501-1
Qy
                                                   B
                                                                                                                                                       Вþ
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Physcomitrella patens US-09-734-017A-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-734-017A-54
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Best Local Similarity
Watches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1/WordPerfect
SEQ ID NO 54
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Frank, Markus
APPLICANT: Freund, Annette
APPLICANT: Duwenig, Elke
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involv
TITLE OF INVENTION: the sis of amino acids, vitamins, cofactors, nucleotides an
TITLE OF INVENTION: nucleosides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: synthesis of amino acids, TITLE OF INVENTION: nucleosides FILE REFERENCE: BASF-NAE-1331-99-US CURRENT APPLICATION NUMBER: US/09/734,017A CURRENT FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lerchl, APPLICANT: Renz,
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/171,100 PRIOR FILING DATE: 1999-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 SASLANSNPPPPTASLGT--LISLFGRQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDT 205
133 PTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLEGRQ-GLSPRDMTALSGAHTIGQ 191
                                                   53 TGGP-LGTIRFGQELAHGANAGLDIAVNLLQPIKEQFP-ELSYADFYTLAGVVAVEVTGG 110
                                                                                                   84 TAGPNLNSVR------GFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGG 132
                                                                                                                                                                                  30 ASSCPNIQSIVRAAMTQA-----VASEQRMGASLLRLFFHDCFVQGCDGSILLDAGGEK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 NAGLKIAIDLLEPIK-----AKHPKITYADLHQLAGVVAVEVTGGPTVEFIPGRRDS--- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 NLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTA 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 LQSIVRAAMT-QAVASEQRMGASLLRLFFHDCFVQ-----GCDGSILLDAGGEKTAGP 87
                                                                                                                                                    2 AKSYPNVSEKYAALIEKARRKIRGMVAEKNCAPIILRLAWH------GSGTYDQ-ESK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SVCPREGRLPDAKKGAPHLRDIFYRMGLTDKDIVALSGGHSLGKAH----
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Ehrhardt, Thomas
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                                                                                                                                                                                                                                                                                8.5%;
29.0%;
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                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                     Score 136; DB 10;
Pred. No. 1.4e-05;
5; Mismatches 71;
                                                                                                                                                                                                                                                                                                      Length 176;
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US-10-095-975-2
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; TYPE: PRT
; ORGANISM: Bjerkandera
US-09-885-329-6
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US-09-885-329-6
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APPLICANT: MCARdle, Barbara
TITLE OF INVENTION: Polypeptides Having
TITLE OF INVENTION: And Mucleic Acids
FILE REFERENCE: 10048.200-US
FULRENT APPLICATION NUMBER: US/09/885,:
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 09/596,824
PRIOR FILING DATE: 2000-06-19
                                                                                                                                                                       Sequence 2, Application US/10095975 Publication No. US20030013182A1 GENERAL INFORMATION:
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Best Local
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Patent No. US20020115170A1
                                                                              APPLICANT: Yaver, Debbie S.
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Isolating
TITLE OF INVENTION: Microorganisms
FILE REFERENCE: 10160.200-US
PRIOR APPLICATION NUMBER: 06/275,283
PRIOR FILING DATE: 2001-03-17
                                           CURRENT APPLICATION NUMBER: US/10/095,975
CURRENT FILING DATE: 2002-03-12
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                      264
                                                                                                                                                                                                                                                                                                                         257 DQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVG 295
                                                                                                                                                                                                                                                                                                                                                                                                           218 TCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSRRGLFH---
                                                                                                                                                                                                                                                                                                                                                                                                                                               173 APFDTVDAIIARFADVDFSVDEIVALLASHSVAAAS------HIDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 PPTASLGTLISLEGRQGLSPRDMTALSGAHTIGQARCTTERGRIYGDTDINASFAALRQQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 QKPYITKYNMTPG-----DVVQFAGAVGLSNCPGAPQLEFLLGR---TAATAASPTGLIP
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Local Similarity 24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 SLRLTFHDAIGYSPALAAAGSFAGGGADGSILTFSDVEAAFFANAGLD-----EMIEL 120
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                                                                                                                                                                                                                                                                                                                                                                       TVPES-----PLD-STPGVFDTQFFVE-TSLNGTMYPGTSGNIGEALSAIAGELRLLS
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US-09-748-264A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin
SEQ ID NO 2
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 376
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                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A BASIDIOMYCETE PEROXIDASE GENE-TRANSFERRED PLANT TITLE OF INVENTION: DECOMPOSING AND REMOVING NOXIOUS CHEMICALS USING FILE REFERENCE: 04863.0050
CURRENT APPLICATION NUMBER: US/09/748,264A
CURRENT FILING DATE: 2000-12-27
CURRENT FILING DATE: 2000-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2000-223653 PRIOR FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SECRETARY OF AGENCY OF INDUSTRIAL SCIENCE AND TECHNOLOGY APPLICANT: YOSUKE IIMURA
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Coriolus versicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 365
                                                            111 NLGYDEIIDEQRPFIARHNLTTADFIQFAGAIGVSNCPGAPQLDVFIGRPDATQPAPDL-
                                                                                                    101 ---IKRNVEAACPGV----VSCADILALAARDG-TNLLGGPTWSVPLGRRDSTTASASLA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
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                                                                                                                                                                                                                                 1 MAFKTL-----ASLLSVLVTIQVASGALTRRVACPDGVNTATNAACCQLFAVRDDIQQN
                                                                                                                                                                                                                                                                           1 MASPTLMQCLVAVSLLSCVAHAQLSPTFYAS--SCPN-LQSIVRAAMTQAVASEQRMGAS
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NSNPPPPTASLGTLISLFG-RQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASF
                                                                                                                                                                                         L------LRLFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDT---- 100
                                                                                                                                              LFDGGECGEEVHESLRLTFHDAI -- GISPSIA -- SRGQFGGGGADGSIALFEDIETNFHA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOTPVRFDTAYFTNLL 248
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                                                                                                                                                                                                                                                                                                                   7.8%; Score 125.5; DB 10; 25.1%; Pred. No. 0.00041; ive 34; Mismatches 112;
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GENERAL INFORMATION:
APPLICANT: Yaver, Debbie
APPLICANT: McArdle, Barbara
TITLE OF INVENTION: Polypeptides Having
TITLE OF INVENTION: And Nucleic Acids
FILE REFERENCE: 10048-200-US
FULRENT APPLICATION NUMBER: US/09/885;
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 09/596,824
PRIOR FILING DATE: 2000-06-19
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US-09-885-329-2
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APPLICANT: Yaver, Debbie
APPLICANT: McArdle, Barbara
                                                                                                                                                                                                      Sequence 4, Application US/09885329 Patent No. US20020115170A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09885329 Patent No. US20020115170A1
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CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 09/596,824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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NUMBER OF
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                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                      261 FNGGSQDALVRQYSASASLFNADFVAAMIRMGNVG-VLTGTAGQIR 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 VAHQSLRLTFHDAVAFSPALTAQGQFGGNGADGSIITFGDIETAFHPNI----GLDEIVA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLLAALSVAIFLGTAQGMLSTPRVACPDGVNTATNAACCALFAVRDDIQANMFDGGQCND
                                                                                                                                                                                                                                                                                                                   -TGGDNGA-
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ID NOS:
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                                                                        US/09/885,329
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                                                                                                            Having Peroxidase
Acids Encoding Sar
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Query Match
Best Local Similarity
71; Conserve
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                                                                                                                                                                                                                                               SEQ ID NO 12
LENGTH: 372
TYPE: PRT
ORGANISM: Phanerochaete chrysosporium
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SEQ ID NO 4
                                                                                                                                                                                Matches
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020138878A1
                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: 60/242,408
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/981,900B CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TRANSGENIC PLANTS TITLE OF INVENTION: AND CELLULOSE TO FILE REFERENCE: MSU 4.1-539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sticklen, Masomeh APPLICANT: Magbool, Shahina
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn ve
                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
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                                                                                47 AVASEQRMGASLLRLFFHDCFV--
                                                                                                                                                                                              Local Similarity
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GFEVIDTIKRNVEAACPGV----VSCADILALAARDG-TNLLGGPTWSVPLGRRDSTTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKRNVEAACPGVVSCADILALAARDG-TNLLGGPTWSVPLGRRDSTTASASLANSNPPPP 159
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                                                    AEAHE-----ALRMVFHDSIAISPKLQSQGKFGGGGADGSIITFSSIETTYHPNI----
                                                                                                                                               QCLVAVSLLSCVAHAQLSPTF-YASSCPN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LRLFFHDCF------VQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDT 100
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                                                                                                                  QLLAALSVALTLQVTQAAPNLDKRVACPDGVHTASNAACCAWFPVLDDIQQNLFHGGQCG
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                                                                                                                                                                                               Score 104.5; DB 10; Pred. No. 0.046;
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Pred. No. 0.0084;
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                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTAINING LIGNINASE AND CELLULASE WHICH FERMENTABLE SUGARS
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                                                                                    -QGCDGSILLDAGGEKTAGPWLNSVR
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                                                                                                                                                                                  Indels
                                                                                                                                                  ----LQSIVRAAMTQ 46
                                                                                                                                                                                                               Length 372;
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                                                                                                                                                                                  87;
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RESULT 12
US-10-101-464A-802
Sequence 802, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhulzen, Nicolaas
APPLICANT: Higgins, Colleen M.
ITTLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: And Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-981-900B-14
; Sequence 14, Application US/09981900B
; Patent No. USS/0020138878A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/242,408
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 14
LENGTH: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sticklen, Masomeh B
APPLICANT: Madpool, Shabina B
APPLICANT: Madpool, Shabina B
APPLICANT: Madpool, Shabina B
APPLICANT: Dale, Bruce E
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH DEGRAD
TITLE OF INVENTION: AND CELLULOSE TO FERMENTABLE SUGARS
FILE REFERENCE: MSU 4.1-39
CURRENT APPLICATION NUMBER: US/09/981,900B
CURRENT FILLING DATE: 2002-03-18
   PRIOR APPLICATION NUMBER: 09/704,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 LGTLIS-LFGRQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 QKHGVTPG-----DFIAFAGAVALSNCPGAPQMNFFTGRAPATQPA----PDGLVPEPFHS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 DPTISGL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 ---PDGLVPEPFHTIDQVLARMLDAGGFDEIETVWLLSAHSIAAA------NDV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GLDEVVAIQK-----PFIAKHGVTRGDFIAFAGAVGVSNCPGAPQMQFFLGRPEATQAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                           257 GEMRLQSDFLIA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 ----FNADFVAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 NYEAACPGVVSCADILALAARDG-TNLLGGPTWSVPLGRRDSTTASASLANSNPPPPPTAS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 IRLVFHDAIAISPAMEPQASSVRGADGSIMIFDEIETNFHPNI----GLDEIVRLQKPFV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 LRLFFHDCF------VQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKR--- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDQIIDRVFDAGEFDELELVWMLSAHSVAAA-----NDIDPNIQGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGDGNLAPIDVQTPVRFDTAYFTNL~LSRRGLFHSDQELFNGGSQDALVRQYSASASL- 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PFD-STPGIFDSQFFVETQLAGTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 5.6%; Score 89.5; l Similarity 22.6%; Pred. No. 1. 57; Conservative 32; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------PFD-STPGQFDSQFFVETQLRGTAF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                            APPLICANT: Delagrave, Simon
APPLICANT: Murphy, Dennis J.
APPLICANT: Murphy, Dennis J.
APPLICANT: Marphy, Dennis J.
APPLICANT: Maffa III, Anthony M.
APPLICANT: Bylina, Edward J.
APPLICANT: Bylina, Edward J.
APPLICANT: Coleman, William J.
APPLICANT: Wariant Galactose Oxidase, Nucleic Acid Encoding Same, And TITLE OF INVENTION: Using Same
FILE REFERENCE: HER-0040
CURRENT APPLICATION NUMBER: US/09/782,906
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/185,001
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 639
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PRIOR APPLICATION NUMBER: 09/228,986
PRIOR EILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR PILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 1990-01-11
NUMBER OF SEQ ID NOS: 989
SEQ ID NO 802
LENGTH: 345
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US-09-782-906-5
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TYPE: PRT
; ORGANISM; Eucalyptus grandis
US-10-101-464A-802
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                                                                                                                                                           ; OTHER INFORMATION: No. US20010051369Alel Sequence US-09-782-906-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09782906 Patent No. US20010051369A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 5.5%; Score 89; DB 9; Length 345; Best Local Similarity 22.8%; Pred. No. 1.3; Matches 65; Conservative 33; Mismatches 107; Indels 80;
                                                      Matches
                                                                            Query Match
Best Local
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 LSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 CGSSPLAACSLSGTSPPASSSLTVPSNPSSMPETPAIGP-----GQKHRQKGLSTGAIVA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 RL-LTLRLQSNLLSGEVPDLSVSLKNLKELNLTNNELYGHLPDGLLRKFGVRSFVGNEGL 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 IALANCVALLYVTSFVVAYCCSRERNSSLKANGESTGKRRSGSSH 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
   64 HDCFVQGC----DGSILLDAG--GEKTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CSAAWRGVRCSSSTHSSSRVTALSIPSIN--LRGPIDSLSSLDQ-----LRLLDLHDNR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 CLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLF-FHDCF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQG-----CDGSILLDAGGEKTAG---PNLNSVRGFEVIDTIKRNVEAACPGYVSCAD 117
                                                   1 Similarity 20.5 63; Conservative
                                                5.3%; Score 84.5; D. 20.5%; Pred. No. 8.6; ative 24; Mismatches
      ----GPNLNSVRGFEVIDTI----- 101
                                                                                                       DB 10;
                                                   Indels 125;
                                                                                                    Length 639;
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                                                   Gaps
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.70 09	31	76 293	26 234		LENGTH: TYPE: P ORGANIS 0-101-4	TWAF	# # F			7 X X X	R	d Dirigit	AL AL	14 01-	05	258	55	12	04	61	344	27	284	102	224
FGRQGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSG 223	GGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISL	LLDAGGEKTAGPNINSVRGFEVIDTIKRNVEAACP-GVVSCADILALAARDGTNIL 130	PTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQGCDGSI 75 {	Match 5.3%; Score 84.5; DB 9; Length 804; Local Similarity 22.6%; Pred. No. 12; Local Similarity 37; Mismatches 122; Indels 47; Gaps 11; es 60; Conservative 37; Mismatches 122; Indels 47; Gaps 11;	LENGTH: 804 TYPE: PRT ORGANISM: Pinus radiata 0-101-464A-890	ND 890 ID NOS: 989 NO 890	ATION N	DATE:	FILING DATE: 2000-11-01 FILING DATE: 1999-01-12	FILING DATE	FERENCE: 11000.1020c2 in the moultication of t	Nieuwenhuizen, Nicolaas Higgins, Colleen M. NVENTION: Compositions Isolated from Plant Cells NVENTION: Compositions Isolated from Plant Cells	ublication No. US20030046728A1 ENERAL INFORMATION: APPLICANT: Strabala, Timothy	4647	GRVFNGG 511	QELFNGG 264	TGGQRRGIPFEDSTPVFTPEIYVPEQDTPYKQNPNSIVRAYHSISLLLPD 504	AALROOTCPRSGGDGNLAPIDVQTPVREDTAYFTNLLSRRGLEHSD 257	DYQDSDATTNAHIITLGEPGTSDNTVFASNGLHFARTFHTSVVLPDGSTFI 454	ASLGTLISLEGRQGLSPRDMTALSGAHTIGQARCTTERGRIYGDTDINASF 211	SVEQAGPSSAMNWYYTSGSGDVRSAGKRQSNRGVAPDAMSGNAVMYDAVKGKILTEGGSD 403	TNLLGGPTWSVPLGRRDSTTASASLANSNPPPPT 160	FTIGGSWSGGVFEKNGEVYSDSSKTWTSLPNAKVNPMLTADKQGLYRSDNHAWLEGWKKG 343	KRNVEAACPGVV\$CADILALAARD	

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RESULT 15
US-09-976-059-14
US-09-976-059-14
Sequence 14, Application US/09976059
Patent No. US20020164747A1
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
FILE REFERENCE: 3019-PCT
CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
SOFTMARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 4999
TYPE: PAT
ORGANISM: Actinoplanes sp.
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Search completed: April 26, 2003, 12:43:24 
Job time : 46 secs
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                                                                                                                                                                                     1795 PAVVGT-----PDGVLPPSFYLDVGGDVLPGDLARRWLRDGRVLFNSYGPTETTVNAAT 1848
                                                                                                                                                                                                                                                                                                                                                                          1740 RVAQFASPGFDMFVDEWSMAL-----LAGAALTFVPPERRLGADLAAFLAEYGVTHATLP 1794
                                                                                               1901 LNRAGLTAERFVACPFEPGERMYRTGDV 1928
                                                                                                                                                                                                                                                                                                                                                                                                                    103 RNYEAACPGVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLAN----SNPPPP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 LDGSIPELNGSCPELSFFSVHTNKLS 494
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                                                                                                                                       274 SASASLENADEVAA-----MIRMGNV 294
                                                                                                                                                                                                                                                                                                                            160 TASLGTLISLFGRQGLSPRDMTALSGAHTI -- GQARCTTFRGRI---- YGDTDINASFAA 213
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL-frame+_p2n.model -DEV=x1h
-Q-/cgn2_1/USPTO_spool/US10047825/runat_26042003_112042_7644/app_query.fasta_1.455
-Q-/cgn2_1/USPTO_spool/US10047825/runat_26042003_112042_7644/app_query.fasta_1.455
-DB-GenEmbl -QFMT-fastap -SUFFIX=rge -MINATCH=0.1 -LOOPCLF0 -LOOPEXT=0
-UNITS-bits -START-1 -END=-1 -MARIX=01190 -TRANS-human40.cdi -LIST-45
-DCCALIGN=200 -THR_SCORE-quality -THR_MIN=16 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10047825_eCGN_1_1_168_erunat_26042003_112042_7644 -NCPU=6 -ICPU=3
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-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
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33: em_htg_mus:*
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36: em_htg_nam:*
37: em_htg_other:*
40: em_htg_other:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.

Score

Query Match

Length

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Description

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ALIGNMENTS

RESULT 1

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RESULT 2
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                                                                            LeuValArgGlnTyrSer 274
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Submitted (15-JUL-1994) Annette H. Ross, University of Queensland,
Botany, St. Lucia, Brisbane, Queensland, 4072, Australia
Location/Qualifiers
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Cenchrus ciliaris
Cenchrus ciliaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Paniceae; Cenchrus.
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Thesis (1994) Botany, University of Queensland
2 (bases 1 to 1335)
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SLGTLISLFGGRLSARDMIALSGAHHAQARCTTFFGRIYGDTNIDASFAALQQOTCPR
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127. .978
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440 c 374 g
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FNSDFYAAMIKMGNIGANAGQVRRNCRVVNS"
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/clone_lib="lambda gt-10"
1..57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /EC_number="1.11.1.7"
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RESULT 3 AF149279 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 124 <i>I</i> Db 77676 C	Qy 104 I Db 77736 I	US-10-047-8	Alignment Sc Pred. No.: Score: Score: Percent Simi Best Local S Query Match: DB:	BASE COUNT ORIGIN	source	PPARTITOR O	COMMENT	TITLE JOURNAL	JOURNAL REFERENCE AUTHORS	AUTHORS TITLE	ORGANISM	VERSION KEYWORDS SOURCE	LOCUS DEFINITION ACCESSION
AF149279 Phaseolus vulgaris peroxidase 4 precursor (FBP4):mRNA, partial cds. AF149279 AF149279 AF149279.2 GI:6573300 . Phaseolus vulgaris. Phaseolus vulgaris Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arg 124 CGC 77674	AsnValGluAlaAlaCysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAla 123 	825-4 (1-313) x AP005613 (1-160562) .	Scores: 1.61e-10 Length: 160562 21.00 Matches: 21 milarity: 100.00% Conservative: 0 Similarity: 100.00% Mismatches: 0 h: 6.71% Indels: 0 Gaps: 0	45817 a 33079 c 35854 g 45760 t 52 others	1160562 Vorganism= Toryza sati /cultivar="Nipponbare /db_xref="taxon:39947 /chromosome="2"	and the accession number will be preserved. Phis is a 'working draft' sequence. Sequence will be replaced finished sequence as soon as it is available and ression number will be preserved.	305-8602, Japan rc.go.jp, URL:http://rgp.dna.af 81-298-38-7468) sts of 1 contigs. Gaps between of N. The order of the pieces i however the sizes of the gaps b hat have provided by the submit d by the finished sequence as a	Direct Submission Submitted (01-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai	Published Only in Database (2002) 2 (bases 1 to 160562) Sasaki.T. Watsumoto.T. and Katavose.Y.	Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC clone:OSJNBa0082C09		AP005613.1 GI:22091085 HTG; HTGS: PHASE2. OTYZA SATIVA (Japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBa0082C09.	

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REMARK
COMMENT
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                                                                                                                                                                                                                                                          Submitted (14-DEC-1999) Biochemistry, Royal Holloway, University London, Egham, Surrey TW20 OEX, United Kingdom Sequence update by submitter On Dec 14, 1999 this sequence version replaced gi:5002345.
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Blee, K. A., Jupe, S.C., Richard, G. and Bolwell, G.P.
Molecular cloning and differential expression of six members
peroxidase family in French bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blee, K A ...... (10-MAY-1999) Biochemistry, Royal Holloway, United Kingdom
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                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                               p15a gene; peroxidase.
thale cress.
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AJ006961.1 GI:3242069
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                Justesen, A.F.
                                                                                              Arabidopsis thaliana
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Justesen, A.F., Jespersen, H.M. and Welinder, K.G. Analysis of two incompletely spliced Arabidopsis cDNAs encoding novel types of peroxidase processing Biochim. Biophys. Acta 1443 (1-2), 149-154 (1998)
                                                                                                 Sequence
Ax412410
Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Syngenta Participations AG (CH); UNIVERSITY OF NORTH CAROLINA AT
CHAPEL HILL (US); Glazebrook, Jan (US); Wang, Xun (US); Dangl,
Jeffrey L. (US); Eulgem, Thomas (US)
Location/Qualifiers
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Brassicaceae; Arabidopsis.
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Oestergaard,L., Abelskov,A.K., Jensen,R.B., Hansen,
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Hansen, L.N. and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Sequence 342 from Patent
AX412578
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Syngenta Participations AG (CH); UNI
CHAPEL HILL (US); Glazebrook, Jan (U
Jeffrey L. (US); Euigem, Thomas (US)
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Syngenta Participations Ag (CH); UNYERSI
CHAPEL HILL (US); Glazebrook, Jan (US);
Jeffrey L. (US); Eulgem, Thomas (US)
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Arabidopsis thaliana clone 23349
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Matches:
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Onpublished

(Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Cheuk, R., Chen, H., Kim, C.J., M., Goldsmith, A.D., Hayashizaki, Y.,
Bowser, L., Carninci, Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Bowser, L., Carninci, Dale, J.M., Karlin-Neumann, G.,
Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nayen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Pavis.R.W., Theologis, A. and Ecker, J.R.
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Arabidopsis.
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                           Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Lacr ecotypes and therefore
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Cheuk,R., Chen,H., Kim,C.J., Koesema,E.,
                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                     Arabidopsis cDNA clones
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/db_xref="taxon:3702"
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LQGFEVIDNAKTQLEAACPGVVSCADILALAARDTVILTQGTGWQVPTGRRDGRVSLA
SNANNLPGPRDSVAVQQQKFSALGLNTRDLVVLVGGHTIGTAGCGVFRNRLFNTTGQT
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/protein_id-"AAM64354.1"
/db.xref="Gi:21592403"
/translation="MGLVRSLCLLITELNCLVISVHGQATARPGPVSGTRIGFYLTTC
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RESULT 13
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Query Match:
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                                                                  cationic peroxidase.
A.hypogaea, cDNA to mRNA.
Arypogaea, cDNA to mRNA.
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoidcae;
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Aeschynomeneae; Arachis.
1 (bases 1 to 1330)
                                                                                                                                                                                                                                                                                                                                                        A.hypogaea cationic
M37637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-OCT-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                                                                                                                                                                                                                               M37637.1
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/translation="MGLVRSlcll"
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/db_xref="taxon:3702"
/chromosome="5"
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Gossypium hirsutum bacterial-induced gaiacol peroxidase (pod29)
mRNA, complete cds.
AP485258
AP485268.1 GI:19698451
                                                                                                                                                                                                                                           Gossypium hirsutum.
Gossypium hirsutum.
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
Lobases I to 1389)
                                                                                                                                                              Delannoy, E., Assigbetse, K., Jalloul, A., Marmey, P., Daniel, J.-F., Geiger, J.-P. and Nicole, M.
Direct Submission
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Institut des Sciences Vegetales
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Molecular cloning of complementary DNAs encoding two cationic peroxidases from cultivated peanut cells
Proc. Natl. Acad. Sci. U.S.A. 87 (22), 8874-8878 (1990)
                                                                                                               Submitted (20-FEB-2002) UR Resistance, Montpellier 34032, France
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Location/Qualifiers
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(bases 1 to 1400)

Justesen,A.F., Jespersen,H.M. and Welinder,K.G.
Analysis of two incompletely spliced Arabidopsis cDNAs encodin novel types of percyidase
Biochim, Eiophys. Acta 1443 (1-2), 149-154 (1998)

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1 (bases 1 to 1400)

Wellinder, K.G., Jespersen, H.M., Kjaersgaard, I.V.H., Justesen, A.F., Oestergaard, I., Abelskov, A.K., Jensen, R.B., Hansen, L.N. and Rasmussen, S.K.
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Arabidopsis thaliana
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Justesen, A.F.
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Search completed: May 3, 2003, 14:34:30 Job time: 2215 secs
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protein identification; signal transduction pathway;
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     (CCR), phenylalanine ammonia-lyase (PAL), 4-commarate:COA ligase coniferol glucosyl transferase (CGT), coniferin beta-glucosidase laccase, peroxidase, ferulate-5-hydroxylase (FSH), alpha-amylase, caffeic acid methyl transferase, caffeoyl COA methyl transferase, commerate COA ligase, cytochrome P450 LXXIA, diphenol oxidase, fl glucosyl transferase, flavenoid hydroxylase, and isoflavone reduc
                                                                                                                                             encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
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14-JUL-1999;
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Pinus radiata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinus radiata peroxidase nucleotide sequence SEQ ID NO:366.
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                                                                                                                                                                                                                                                                                                                                                        polynucleotide encoding enzymes involved in lignin-biosynthetic ay useful for producing transgenic plants especially eucalyptus ine species having altered lignin content, composition and
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FLETCHER
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99US-0143811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lignin biosynthetic pathway; Eucalyptus grandis;
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R CHALLENGE FORESTS
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(CBG),
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which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lignin biosynthetic pathway, and for producing a plant having altered lignin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any organism and for PCR amplification. The lignin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAA6149 represent polynucleotide and protein sequences used in the exemplification of the present invention.
Sequence 364 BP;
98 A; 111 C;
  69
G;
86 T; 0 other;
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Alignment Scores: Pred. No.:
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                        Percent Similarity:
                                 Score:
                 Local Similarity:
2.45e-07
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Length:
Matches:
Conservative:
Mismatches:
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US-10-047-825-4 (1-313) x AAA68190 (1-364)

밁 δÃ 182 51 AlaLeuSerGlyAlaHisThrIleGlyGlnAlaArgCysThrThrPheArg GCACTCTCGGGAGCTCATACGATTGGCCAAGCGCGGTGCACCACATTCAGA 101 198

RESULT 5

AAA68156 standard; DNA; 512 ВP

XPXPX AAA68156,

24-OCT-2000 (first entry)

Eucalyptus grandis peroxidase nucleotide sequence SEQ IL NO:249

Pinus radiata; Monterey pine; Plant; lignin; lignin biosynthetic pathway; Eucalyptus ds grandis;

Eucalyptus grandis

20-APR-2000

06-OCT-1999; 99WO-NZ00168

09-OCT-1998; 14-JUL-1999; 98US-0169789. 99US-0143811.

Bloksberg LN, Havukkala IJ;

(GENE-)

GENESIS RES & DEV CORP LTD. FLETCHER CHALLENGE FORESTS LTD

WPI; 2000-317962/27

Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and

Claim 1; Page 133; 213pp; English

The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-commarate:COA ligase (4CCC), coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBC) laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, proteins (CBG)

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XX AAAA6
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DT 20-P
DN WO20
CCB PAAA6
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               The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase
                                                                                  Claim
                                                                                                                              Novel polynucleotide encoding enzymes involved pathway useful for producing transgenic plants and pine species having altered lignin content,
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14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pinus radiata.
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radiata;
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FLETCHER CHALLENGE FOR
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Monterey pine;
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99US-0143811.
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   alcohol dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biosynthetic pathway; Eucalyptus grandis
ey pine; ds.
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                                                                                                                                  in lignin-biosynthetic especially eucalyptus composition and
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Claim 1;

Page

183;

213pp; English

describes isolated

polynucleotides

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Best L
Query
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Pred. No.:
                                                                 Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
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14-JUL-1999;
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                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                      06-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                      Eucalyptus grandis
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99US-0143811.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase CC (OMT), cinnamyl alcohol dehydrogenase (PNL), O-methyl transferase CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (ACL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, CCC caffeic acid methyl transferase, caffeoyl COA methyl transferase, CCC coumerate COA ligase, cytochrome P450 LXLA, diphenol oxidase, flavanol CCC glucosyl transferase, flavanoid hydroxylase, and isoflavone reductase, CCC vhich are involved in the lignin biosynthetic pathway. The CCC composition and the structure of a plant, especially eucalyptus and pine CCC consistion and the structure of a plant, especially eucalyptus and pine CCC pecies, and for modifying the activity of an enzyme involved in lignin CCC to the composition and structure. They can be used for designing probes CCC and primers useful for detecting similar DNA and RNA sequences in any CCC and primers useful for detecting similar DNA and RNA sequences in any CCC and primers useful for detecting similar DNA and RNA sequences in any CCC and primers useful polynucleotides and protein sequences used in the CCC AAB16449 represent polynucleotide and protein sequences used in the CCC axemplification of the present invention.
                                                                                                               30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                 30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                environmental stress
                                                                                                                                                                                                                                             (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peroxidase; active oxygen resistance; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH45565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peroxidase related DNA fragment SEQ ID 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCCTGGGGTCGTCTTGCGCCGACATCTTGGCCTTGGCCGCTCGGGAT
                                                                                 4; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                           23pp; Japanese
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This invention relates to a peroxidase derived from a Paraquat resistant callus. Included in the invention are the gene encoding the peroxidase, a vector containing the gene, and a method for the preparation of the

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AAC45025
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                                                                                                         19-APR-1
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                                                                                                                                                                                                                                                                                                                                Hybridisation assay; ger protein identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peroxidase. The gene is useful for the development of a plant highly resistant against active oxygen which is formed under various environmental stress conditions. This sequence represents a peroxidar related DNA fragment.
                                                                                                                                                                                                                                                         25-FEB-2000;
                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                        metabolic pathway; promoter; termination sequence; ss
                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ
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on; signal transduction pathway;
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9908-0137528 9908-0137528 9908-0137724 9908-0138094 9908-0139452 9908-0139455 9908-0139456 9908-0139456 9908-0139461 9908-0139461 9908-0139461 9908-0139461 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0140353 9908-0144333 9908-0144333 9908-0144333 9908-0144333 9908-0144333 9908-0144333 9908-0144333 9908-0144333 9908-0144333 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145086	13535 13562 13602 13639 13678
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RESULT 1:
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FT S19,
FT MAT 519,
FT MAT 620S

FT PO1.

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28-OCT-1999;
29-OCT-1999;
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                      cDNA clones (AAT66684-87) respectively code for soybean peroxidases SEPal, SEPa2, SEPb1 and SEPb2 (AAM16607-10). Plant peroxidase specific primer SEP (AAM66679) was generated from the conserved distal haem ligand (AAM16603) in all plant peroxidases, and was used to generate a peroxidase gene probe. Primary hybridisation screening using the probe yielded 25 clones. Il Positive clones were recovered after 2 rounds of PCR using PSP and a T7 vector.
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waste disposal; soil reclamation;
                                                                                                                                                                                                                Claim 16; Page 43-44; 63pp; English.
                                                                                                                                                                                                                                                          Isolated soybean peroxidase genes - useful for developing for quantification and monitoring of peroxidase activity
                                                                                                                                                                                                                                                                                                                                    WPI; 1997-259011/23.
P-PSDB; AAW16610.
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  primer,
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    4 clones,
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1126..1130
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Matches:
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    and SEPb2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analysed. The soybean peroxidase genes can be used to develop products for the quantification and monitoring of peroxidase activity, e.g. in assays such as ELISA, PCR, plant breeding programmes, pulp and paper bleaching, on-site waste destruction, soil remediation and organic synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1167 BP; 385 A; 232
        This cDNA clone codes for novel soybean peroxidase SEPb2 (see AAW67734). 4 Clones, designated SEPb1, SEPb2, SEPb1 and SEPb2 (see AAV81420-23) were isolated from a soybean cv. Resnick seedling cDNA library using a plant peroxidase specific primer (see AAV81424) and 3'RACE, Genomic clones (see AAV81418-19) for SEPal and SEPb1 were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV81423;
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                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                               Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No . :
                                                                                             New soybean peroxidase genes - useful, e.g. in pulp and paper bleaching, on site waste destruction and soil remediation
                                                                                                                                                            Vierling
                                                                                                                                                                                                      04-JUN-1997;
                                                                                                                                                                                                                                                                                                   polyA_signal
                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   pulp;
                                                                                                                                                                                                                                                                                                                                                                                                                              Peroxidase;
                                                                        Example 8; Page 48-49; 78pp; English.
                                                                                                                             WPI; 1999-070273/06
P-PSDB; AAW67734.
                                                                                                                                                                                 (INDI-) INDIANA
                                                                                                                                                                                                                           04-JUN-1998;
                                                                                                                                                                                                                                                                      WO9855629-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1998
  obtained.
                                                                                                                                                                                                                                                                                                                                                                                                                   paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-313)
                                                                                                                                                                                                                                                                                                                                                                                                                   SEPb2; soybean; transgenic plant; immunoassay; bleaching; bioremediation; soil decontamination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                       97US-0868577
                                                                                                                                                                                                                           98WO-US11421
                                                                                                                                                                                                                                                                                                                                            /*tag=
39..101
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102..977
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1126..
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 39..980
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17.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA; 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEPb2 cDNA
  coding
                                                                                                                                                                                                                                                                                            g= c
..1131
lg= d
                                                                                                                                                                                  IMPROVEMENT ASSOC
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   regions of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-1167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ი</u>
   SEPa1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319
                                                                                                                                                                                                                                                                                                                                                                                                                      soil decontamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Τ,
   and SEPa2 exhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Best Local Si
Query Match:
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RESULT 12
AAV69276
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Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-047-825-4 (1-313) x AAV81423 (1-1167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                         3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid identity, the coding regions of SEPb1 and SEPb2 share 95% mmino acid identity, and the coding regions of SEPa1 and SEPb1 share 47% amino acid identity. The peroxidases are useful in pulp and paper bleaching, on-site waste destruction, soil remediation, organic synthesis and diagnostic chemistries. Soybean peroxidase has advantages over chlorine bleach, being cheaper, more environmentally friendly, and producing hydroxyl lons with twice the oxidising power of chlorine ions. The plant enzyme is cheap and easy to produce. The invention also relates to immunoassays or
                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                             Soybean
        cDNA encoding soya peroxidase SEPal - useful for producing recombinant peroxidase
                                                                          Vierling
                                                                                                                      27-OCT-1995;
                                                                                                                                                                   24-NOV-1998
                                                                                                                                                                                        US5840558-A
                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                            Glycine max.
                                                                                                                                                                                                                                                                                                                            5'UTR
                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                               Soybean peroxidase SEPb2 polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV69276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV69276 standard; cDNA; 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligonucleotide assays which utilise soybean peroxidase as marker.
                                                                                                (INDI-)
                                                                                                                                             27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                 industry; diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1167 BP; 385 A;
                                         1999-034041/03.
DB; AAW81496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAsp 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCCAGGTGTGGTCTCTTGTGCTGACATCCTTGCTCTAGCAGCAAGGGAT 419
                                                                                                 INDIANA
                                                                                                                                                                                                                                                                                                                                                                                             peroxidase;
                                                                          RA
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                      95US-0671320
                                                                                                                                            95US-0671320
                                                                                                CROP IMPROVEMENT ASSOC.
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978..1167
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102..977
                                                                                                                                                                                                                                                                    /product=
39..101
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/*tag= b
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                                                                                                                                                                                                                                                                                                               *tag=
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17.00
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100.00%
5.43%
                                                                                                                                                                                                                                                                                                                                                                                         SEPal; SEPa2; SEPb1; SEPb2; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                chemistry; ss
                                                                                                                                                                                                                                     ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 C;
                                                                                                                                                                                                                                                                              "SEPb2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 G; 319 T; 0 other;
                                                                                                                                                                                                                                                                            polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-047-825-4 (1-313) x AAV69276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                   Peroxidase derived from Paraquat-resistant callus, it, used for the development of plants resistant t
                                                                                                                                                                                                   30-SEP-1999;
                                                                                                                                                                                                                                                              JP2001095585-A
                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                      Peroxidase; active oxygen resistance; transgenic plant; environmental stress; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAH45561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA encodes a soybean peroxidase SEPb2 polypeptide. The invention provides four cDNA sequences (AAV69273 to AAV69276) encoding soybean peroxidases SEPa1, SEPa2, SEPb1 and SEPb2 (AAW81493 to AAW81496) respectively. An expression vector containing the SEPa1 cDNA sequence can be used to transform host cells for the recombinant production of the peroxidase. The peroxidase is useful in industries and diagnostic
                                                                                                                                                  P-PSDB; AAG64621
                                                                                                                                                            WPI; 2001-360494/38
                                                                                                                                                                               (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                       30-SEP-1999;
                                                                                                                                                                                                                                           10-APR-2001.
                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH45561 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1167
                                                                                                                                                                                                                                                                                                                                                                                   Peroxidase gene
                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Columns 35-38; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No . :
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B₽;
                                                                                                                                                                                                   99JP-0279690
                                                                                                                                                                                                                       99JP-0279690
                                                                                                                                                                                                                                                                                                   Location/Qualifiers 49..1041
                                                                                                                                                                                                                                                                                 /product= "Peroxidase"
                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 A; 232
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17.00
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100.00%
5.43%
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 1191 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-1167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 G; 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1167
17
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                                                                                                                             and gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
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This invention relates to a peroxidase derived from a Paraquat callus. Included in the invention are the gene encoding the per a vector containing the gene, and a method for the preparation peroxidase. The gene is useful for the development of a plant by resistant against active oxygen which is formed under various environmental stress conditions. The present sequence represent

from a Paraquat resistant encoding the peroxidase, the preparation of the

a plant highly

peroxidase gene of the invention.

Claim 3; Page 13-15; 23pp;

Japanese.

formed under environmental stress

ç

active

oxygen

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RESULT 14
AAH45568
ID AAH45568
AC AAH45
XX AAH45
XX PER4
XX PER4
XX PER70
XX N1cot
X
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Best Local Similarity:
Query Match:
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                                                                                                                             Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                US-10-047-825-4 (1-313) x AAH45568
                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                       callus. Included in the invention are the gene encoding the peroxidase, a vector containing the gene, and a method for the preparation of the peroxidase. The gene is useful for the development of a plant highly resistant against active oxygen which is formed under various environmental stress conditions. This sequence represents a PER4 peroxidase related cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1191
                                                                                                                                                                                                                                             Sequence 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-360494/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2001095585-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peroxidase; active oxygen resistance; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PER4 peroxidase related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH45568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH45568 standard;
                                                                                                                                                                                                №
...
                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a peroxidase derived from a Paraquat resistant
                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 20-21; 23pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peroxidase derived from Paraquat-resistant callus, and gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TOYT ) TOYOTA JIDOSHA KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 CysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAsp
                    408
                                                                                                                                                                                                                                                                                                                                                                                                                                    used for the development of plants resistant to med under environmental stress -
                    TGTCCTGGAGTTGTTTCCTGTGCTGATATTCTTGCTCTAGCTGCTCGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                             BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0279690
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                                                                                                            7.79e-07
17.00
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22
                                                                                                                                                                                                                                             364 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       x AAH45561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
                                                                                                                                                                                                                                             238 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ç,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-1191)
                                                                                (1-1229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277
                                                                                                                                                                                                                                             273 G;
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                                                                                                                                                                          Length:
Matches:
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                                                                                                            Gaps:
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Conservative:
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Indels:
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Indels:
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                                                                                                                                                                                                                                             354 T;
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AAA68177
 Q
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                                                                              Query Match:
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                                                                                                                                                              Alignment
                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317962/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA68177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA68177 standard; DNA;
                                                                                                                                                                                              Sequence 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200022099-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucalyptus grandis
                                                                                                                                                 No.:
53 ArgMetGlyAlaSerLeuLeuArgLeuPhePheH1sAspCysPheVal
                                                                                                Similarity:
                                                                                                                                                                                                BP;
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99US-0143811
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16.00
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5.11%
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CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate-COA ligase (ACL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase, CC caffeic acid methyl transferase, Caffeoyl CoA methyl transferase, CC coumerate CoA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol CC glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, CC which are involved in the lignin biosynthetic pathway. The CC composition and the structure of a plant, especially eucalyptus and pine CC species, and for modifying the activity of an enzyme involved in lignin CC content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any CC organism and for PCR amplification. The lignin content can be efficiently CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to CC AAB16449 represent polynucleotide and protein sequences used in the CC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (CMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; lignin; lignin biosynthetic pathway; Eucalyptus Pinus radiata; Monterey pine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eucalyptus grandis peroxidase nucleotide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated polynucleotides and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 184; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and pine species having altered lignin content, composition
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FLETCHER CHALLENGE FORESTS LTD
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Length:
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Db 173 CGCATGGGTGCTTCTCTCCTGCGCCTCTTCTTCATGATTGCTTCGTC 220

Search completed: May 3, 2003, 13:57:21 Job time: 194 secs

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US-09-615-192A-366

GENERAL INFORMATION:

APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka

FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR APPLICATION NUMBER: US 08/713,000

TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content FILE REFERENCE: 11000.1003c4U

Sequence 366, Application US/09615192A Patent No. 6410718

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Result
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3: /cgn2_6/ptodata/
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5: /cgn2_6/ptodata/
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-615-192A-366

US-09-615-192A-249

US-09-615-192A-350

US-09-615-192A-350

US-08-671-320-16

US-08-688-577-16

US-09-615-192A-353

US-08-671-320-14

US-08-868-577-14
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2086.735 Million cell updates/sec
                             Sequence 366, App
Sequence 249, App
Sequence 362, App
Sequence 350, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 353, App
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                Sequence
Sequence
   App1
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В γ

US-09-615-192A-249

GENERAL Sequence Patent No.

INFORMATION:

249, Application US/09615192A 5. 6410718

APPLICANT:

APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION: Modification of Plant

Lignin Content for the Bloksberg, Leonard N.

US-10-047-825-4 (1-313) x US-09-615-192A-366 (1-364)

182 AlaLeuSerGlyAlaHisThrIleGlyGlnAlaArgCysThrThrPheArg 198 51 GCACTCTCGGGAGCTCATACGATTGGCCAAGCGCGGTGCACCACATTCAGA

Query Match: DB:

Percent Similarity: Best Local Similarity:

100.00% 100.00% 5.43% 1.92e-08 17.00

Mismatches: Indels: Matches: Conservative:

364 17 0 0

Alignment Scores: Pred. No.:

Score:

; LENGTH: 364 ; TYPE: DNA ; ORGANISM: Pinus r US-09-615-192A-366

SOFTWARE: Fa

NUMBER OF SEQ ID NOS:

FastSEQ for Windows Version 3.0

PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-10-09

us 09/169,789

; TYPE: DNA; Eucalyptus; ORGANISM: Eucalyptus US-09-615-192A-249

grandis

Scores:

SOFTWARE: Fa SEQ ID NO 249 LENGTH: 512

NUMBER OF SEQ ID NOS:

FastSEQ for Windows Version 3.0

405

FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09

Best Local Similarity: Percent Similarity:

2.67e-08 17.00 100.00% 100.00% 5.43%

Length: Matches:

Mismatches: Indels: Conservative:

512 17 0 0

Score: Pred. No.: Alignment

Gaps:

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: NUMBER OF SEQ ID NOS: 405
: SOFTWARE: FastSEQ for Will
: SEQ ID NO 362
: LENGTH: 586
: TYPE: DNA
: ORGANISM: Pinus radiata
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; Sequence 362, Application US/09615192A
; Patent No. 6410718
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; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-350
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CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6410718
GENERAL INFORMATION:
                                                                  SEQ ID NO 350
LENGTH: 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 350, Application US/09615192A
                                                                                                                                                                                                                                          FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US.709/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11 PRIOR APPLICATION NUMBER: US 09/169,789 PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin
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                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, 11ka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
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Query Match:
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Pred. No.:
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               Alignment Scores:
                                            US-08-671-320-16
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 402-398-9005 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: 1125 SO.
STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VIEBLING JR, RICHARD A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
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                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                       NAME/KEY:
                                                                                                                  NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Matches:
Conservative:
Mismatches:
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 Length:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
Percent Similarity:
Best Local Similarity:
                                               Pred. No.:
                                                              Alignment Scores:
                                                                                           ; NAME/KEY:
; LOCATION:
US-08-868-577-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08868577 Patent No. 5866695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOPTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/8
FILING DATE: 04-JUN-1997
CLASSIFICATION: 536
CLASSIFICATION: TURDDBMATTON:
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 402-333-1510
INFORMATION FOR SEO ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vierling Jr., Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
TELEFAX: 402-333-1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Jondle, Robert J.
                                                                                                                                         FEATURE:
                                                                                                                                                                                       FEATURE
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                                                                                                                                                                                                                                                                                                                                              OLECULE TYPE: CDNA
                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 555 13th
CITY: Washington
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555 13th Street NW, Suite 701 East
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102..977
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978..1167
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39..977
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SYSTEM: PC-DOS/MS-DOS
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39..101
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                Conservative:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Eucalyptus grandis US-09-615-192A-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-615-192A-353

: Sequence 353, Application US/09615192A

: Patent No. 6410718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: F
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08671320 Patent No. 5840558
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: VIERLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
             COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 337
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                  ADDRESSEE: 1125 SO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 CGCATGGGTGCTTCTCCTGCGCCTCTTCTTCATGATTGCTTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 ArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheVal
                                                                                                                                             COUNTRY: US
ZIP: 68124-1076
                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                              STREET:
APPLICATION NUMBER:
                                                                                                                                                                                                           CITY: OMAHA
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                                                                                                                                                                                                                                                                                                              VIERLING JR, RICHARD A
VENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
VENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
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US/08/671,320
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Matches:
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Indels:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000

1227-001

TELEPHONE: 402-398-9000
TELEPAX: 402-398-9005
TELEFAX: 402-398-9005
NFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

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US-08-868-577-14
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-671-320-14
                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Vierling Jr., Richard A
APPLICANT: Vierling Jr., Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: 555 13th Street NW, Suite 701 East
                                                                                                                                                                                                                                                                                                                                                                  sequence 14, Application US/08868577 Patent No. 5866695
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
FEATURE:
                                                                            SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/08/868,577
FILING DATE: 04-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                             COUNTRY: U
ZIP: 20004
                                                                                                                                                                                                           STREET: 555 13th
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1191 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
Jondle, Robert J.
                                                                                                                                                                                             USA
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60..998
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999..1191
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1..59
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123..998
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60..122
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-868-577-14
                               Percent Similarity:
Best Local Similarity:
Query Match:
US-10-047-825-4 (1-313) x US-08-868-577-14 (1-1191)
                                                                                              Alignment Scores:
                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                      TELEFAX: 402-333-1510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
TELEPAX: 402-333-1510
                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                            FEATURE:
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60..998
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60..122
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16.00
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                                                                       Length:
Matches:
                                   Mismatches:
Indels:
                                                            Conservative:
                     1191
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Search completed: May Job time : 48 secs 3, 2003, 14:53:14 밁 QΥ

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Run on:

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LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo

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-FGAPDEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Maximum DB
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Perfect score:
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                                                                                                                       Score
                                                                                                                                                                                                                                    d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seg length: 2000000000

    nucleic search, using frame_plus_p2n model

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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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2. /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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US-09-938-842A-1518
US-09-878-574-12464
US-09-878-574-744
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3424.513 Million cell updates/sec
Sequence 1596, Ap
Sequence 1518, Ap
Sequence 12464, A
Sequence 744, App
                                                                                                                       Description
                                        APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1518
LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1518, Application US/09938842A Patent No. US20020160378A1
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     ORGANISM: Arabidopsis thaliana
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Conservative: Mismatches: Indels: Length: Matches:

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Result No.

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				ALIGNMENTS				
ESULT 1 S-09-938-842A-1596 S-09-938-842A-1596 Patent No. US20020160378A1	1596 Applic	eation)378A1	us/o)9938842A				
APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel APPLICANT: Wang Xin	MATION: irper, c (reps, c	reff roel						
APPLICANT: Waity, Auto APPLICANT: Zhu, Tong	thu, Tor	on proce	1 0 50	THE PRES OF	DI NITIO	TONCCENTO	DI ANTIC	CONTATINT
TITLE OF INVE	ENTION:	SAME,	ANI	TITLE OF INVENTION: SAME, AND METHODS OF USE				-
FILE REFERENCE: SCRIP1300-3	E: SCR	P1300-	ω					
CURRENT APPLICATION NUMBER: US/09/938,842A	CATION	NUMBER	: 08	3/09/938,842A				
CURRENT FILING DATE: 2001-08-24	WG DATE:	2001	-08	-24				

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GENERAL

Query Match:

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APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.

FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with CITLE OF INVENTION: Plants

FILE REFERENCE: 38 221(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION UNUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NO.5: 15775

SEQ ID NO.12464

LENCTH: 271

TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701065809H1

US-09-878-574-12464
                                                                                                       APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: NUCLEIC ACID MOLECULES BELIEVED BY APPLICATION NUMBER: US/09/878,574

CURRENT APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION UNBER: 09/333,535

PRIOR FILING DATE: 1999-06-14
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; Sequence 12464, Application US/09878574
; Patent No. US20020110548A1
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                                                                      SEQ ID NO 744
                                                                                                                                                                                                                                                                                                                                 Sequence 744, Application US/09878574 Patent No. US20020110548A1
                                                                                          NUMBER OF SEQ ID NOS: 15775
                              TYPE: DNA
        ORGANISM: Glycine max
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-22
NUMBER OF SEQ ID NO 2663
LENGTH: 993
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2693
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; Sequence 2656, Application US/09938842A

; Patent No. US20020160378A1
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Best Local Similarity:
Query Match:
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patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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Best Local Similarity:
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE REPERENCE: SCRID1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILLING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
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LENGTH:

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Sequence 8092, Application US/09878574

Patent No. US20020110548A1

GENERAL INCOMMATION

APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

FILE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)8

CURRENT APPLICATION UNMBER: US/09/878,574

CURRENT APPLICATION NUMBER: 09/333,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR PILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 8092

LENGTH: 285

TYPE: DNA

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: 701100739H1

US-09-878-574-8092
                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2656
LENGTH: 1074
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Best Local Similarity:
Query Match:
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US-09-878-574-8092
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Pred. No.:
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   OPNB7
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S37495	JQ2217	JU0457	T46118	H84767	860055	S00626	C96532	OPRHC	JC4780	S00627	T03686	T45730	T03912	S14268	JC4781
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ALIGNMENTS

Qy 244 FTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQ : ::: : : : : : : : :	Qy 126 GTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSG	Qy 11 VAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQG 70 : : : : :	Query Match 62.6%; Score 1004.5; DB 2; Length 309; Best Local Similarity 63.1%; Pred. No. 5.7e-74; Matches 195; Conservative 46; Mismatches 61; Indels 7; Ga	C; Superfamily: peroxidase C; Keywords: heme; iron; metalloprotein; oxidoreductase C; Keywords: heme; iron; metalloprotein; oxidoreductase C; Keywords: heme; iron; metalloprotein; oxidoreductase C; Keywords: heme; iron; metalloprotein F; 50/Active site: Arg *status predicted F; 50/Active site: Arg *status predicted F; 56-61/Disulfide bonds: *status predicted F; 110-305/Disulfide bonds: *status predicted F; 189-214/Disulfide bonds: *status predicted	A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residuse: 1-309 <sim> A; Cross-references: EMBL:Y10467 A; Experimental source: subspecies Nobel C; Genetics:</sim>	probable peroxidase (EC 1.11.17) (clone PC23) - spinach (fragment) C;Species: Spinacia oleracea (spinach) C;Date: 11.Jun-1999 #sequence_revision 11.Jun-1999 #text_change 20.Jun-2000 C;Accession: T09166 R;Sinon, P. submitted to the EMBL Data Library, January 1997 A;Reference number: Z16599 A;Accession: T09166
TTGTAGQ 303 :: : TGSSGE 300	DMTALSG 185 MTALSG 180 VREDTAY 243 : TKFDNSY 240	HDCFVQG 70 HDCFVNG 60 LALAARD 125	309; 7; Gaps 3;	predicted		ent) 20-Jun-2000

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peroxidase (EC 1.11.1.7) - flax (fragment)
C:Species: Linum usitatissimum (flax)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_C
C:Accession: 708121
R:Omann, F: 7950n, H.
submitted to the EMBL Data Library, February 1998
A;Description: cDNA sequence of a basic peroxidase (FLXPER
A;Reference number: Z16366
A;Accession: 708121
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-305 < COMA>
A;Cross-references: EMBL:AF049881; NID:g2944416; PIDN:AACO
A;Experimental source: cv. Stormont Cirrus
C:Genetics:
A;Gene: PER4
C:Superfamily: peroxidase
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxi
F:34.181/Binding site: heme iron (His) (axial ligands) #st
F:56-61/Disulfide bonds: #status predicted
F:50/Active site: Arg #status predicted
F:303/CD/Sulfide bonds: #status predicted
F:303/CD/Sulfide bonds: #status predicted
F:303/CD/Sulfide bonds: #status predicted
                                                                                                                                                                 probable peroxidase (EC 1.11.1.7) (clone PC44) - spinach C;species: Spinacia oleracea (spinach) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text C;Accession: T09164
                                                                               submitted to the EMBL Data A; Reference number: Z16599 A; Accession: T09164
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                 A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-323 <SIM>
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A; Cross-references: EMBL:Y10465
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Best Local
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                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VARRGLLHSDQELFNNGTQDALVRTYSNNAATFATDFAAAMVRMGNISPLTGTNGEIRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TIGQARCTTFRQRIYNDTNIDPAFATTRRGNCPQAGAGANLAPLD-GTPTQFDNRYYQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 VLVGGPTWTVPLGRRDARTASQSAANAQIPAPGSSLGTITNLFTNKGLTARDVTILSGAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 NLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 TIGOARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 DGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AMSLLASSGSAQLAANFYATSCPTLLTIVRNAMTQAVNSENRMAASILRLHFHDCFVNGC
                                                                                                                                                                                                                                                                                                                                                                                        CRVVN 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197;
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                                                                                                                         Library,
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                                                              from GB/EMBL/DDBJ
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                                                                                                                            January
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A; Note: prxr4
C; Superfamily: peroxidase
C; Keywords: heme; iron; metalloprotein; oxid
F; 37-118/Disulfide bonds: #status predicted
F; 64/Accive site: Arg #status predicted
F; 64/Accive site: Arg #status predicted
                                                                                       R.Welinder, K.G.

R.Welinder, K.G.

R.Welinder, K.G.

Eur. J. Biochem. 151, 497-504, 1985

Eur. J. Biochem. 151, 497-504, 1985

Eur. J. Biochem. 151, 497-504, 1985

A;Title: Plant peroxidases: their primary, secondary and A;Title: Plant peroxidases: the primary and A;Title: Plant peroxidas
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                                                                                                                                                                                                                                                                                                                                                                      R; Welinder, K.G.; Mazza, G.
Eur. J. Biochem. 73, 353-358, 1977
Eur. J. Biochem. 73, 353-358, 1977
A; Title: Amino-acid sequences of heme-linked, histidine-containing peptides A; Reference number: A91246; MUID:77138218; PMID:849740
A; Accession: A91246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Brassica rapa (turnip)
C;Date: 31-Oct-1980 #sequence_revision
C;Accession: A91994; A91246; B23116; PA
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R;Mazza, G.; Welinder, K.G.
Eur. J. Biochem. 108, 481-489, 1980
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A; Molecule type: protein A; Residues: 'Z', 2-296 <W
                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                       A; Note: these two histidine-containing
                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 32-65; 161-175 <WEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: the protein shown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-296 <MAZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMI 289
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197; Conserv
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                                                                                                                                                                        tertiary structures,
                                                                                                                                                                                                                                                                              essential
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comp1

turni

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peroxidase (EC 1.11.1.7) - radish
C:Species: Raphanus sativus (radis
C:Date: 16-Jul-1999 #sequence_revi
C:Accession: T10252
R:Park, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: peroxidase (Skeywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase; F;11/Modified site: pyrrolidone carboxyllo acid (Gln) #status experimental F;11-91,44-49,97-292,176-201/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: PN0612; MUID:93384622; PMID:8396932
A;Accession: PN0612
A;Molecule type: protein
A;Residues: 'Z',2-32,'AG',35-88,'D',90-156,'K',158-296 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Dlehn, S.H.; Burkhart, W.; Graham, J.S. Biochem. Biophys. Res. Commun. 195, 928-934, 1993 Biochem. Biophys. Res. Commun. 195, 928-934, 1993 A;Title: Purification and partial amino acid sequence of wound-inducible, A;Reference number: PN0612; MUID:93384622; PMID:8396932
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                                                                                                                                                                                                         C;Superfamily: peroxidase C;Keywords: chromoprotein; glycoprotein; heme; iron; oxidoreductase
                                                                                                                                                                                                                                                                A; Gene: prxk1
A; Introns: 68/3; 131/3; 186/3
                                                                                                                                                                                                                                                                                                     A; Experimental source: cultivar Handsome C; Genetics:
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-315 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T10252
                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A; Reference number: Z16998
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                   융
                                                                                                                                                                                                                                                                                                                                           A; Cross references: EMBL: X91172
                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
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                                                                                                          LVAVSLLSCVAHAQLSPTFYASSCRNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARVYNETNINAAFATLRQRSCPRAAGSGDANLAPLDINSATSFDNSYFKNLMAQRGLLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGRRDAKTASQAAANSNIPAPSMSLSQLISSFSAVGLSTRDMVALSGAHTIGQSRCVNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGRRDSTTASASLANSNPPPPTASLGTLISLEGRQGLSPRDMTALSGAHTIGQARCTTER 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLTTNFYSTSCPNLLSTVKSGVKSAVSSQPRMGASILRLFFHDCFVNGCDGSILLDDTSS
                 GCDGSILLDDTSFTGEQNAGPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAIAARDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRIYGDTDINASFAALRQQTCPRS--GGDGNLAPIDVQTPVRFDTAYFTNLLSRRGLFHS
                                                                                      VIVITLLLQGGEAQLTTNFYSTSCPNLLSTVKSGVKSAVSSQPRMGASILRLFFHDCFVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182;
                                                                                                                                                           184;
                                                                                                                                                       h 58.3%; Score 935; DB 2; Similarity 59.9%; Pred. No. 2.5e-68; 84; Conservative 44; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 61.8
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sativus (radish)
#sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.7%; Score 942; DB 1; 61.5%; Pred. No. 6.2e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                             September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                       Hall
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                                                                                                                                                                                           Length 315;
                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peroxidase (EC 1.11.1.7) precursor - rice
C;Species: Oryza sativa (rice)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S22087
R;Reimmann, C; Ringli, C; Dudler, R.
submitted to the EMBL Data Library, June 1992
A;Description: cDNA cloning and sequence analysis of a pathogen-
A;Reference number: S22087
A;Accession: S22087
A;Accession: S22087
A;Accession: S22087
A,Accession: S22087
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S22087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: cv. Nohrin
C;Superiamily: peroxidase
C;Keywords: chromoprotein; heme; iron; metalloprotein;
F;36-111/Disulfide bonds: #status predicted
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A; Residues: 1-317 <REI>
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peroxidase
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              LLRLFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                               KVCGRTN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTIGOSRCTNERTRIYNETNINAAFATLRQKSCPRAAFRRRKPQPLDINSPTSFDNSYFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVQLGGPNWNVKVGRRDAKTASQAAANSNIPAPSMSLSQLISSFRAVGLSTRDMVALSGA
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                                                                                                                                                                                                                                                    RDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGDGNLAPIDVQT
                                                                                      PLIGTOGOIRLSCSKVNS
                                                                                                                                                           PNAFDNAYYSNLLSNKGLLHSDQVLFNGGSADNTVRNFASNAAAFSSAFTTAMVKMGNIS
                                                                                                                                                                                             PVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVG
                                                                                                                                                                                                                                                                                                     186;
(EC
1.11.1.7) - rice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Mismatches
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Pred. No. 9.2e-68;
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A;Cross-references: GB:M37636
C;Superfamily: peroxidase
C;Superfamily: peroxidase
C;Reywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;33-113/Disulfide bonds: #status predicted
F;60/Active site: Arg #status predicted
F;64,191/Binding site: heme iron (His) (axial ligands) #status predicted
F;66,71/Disulfide bonds: #status predicted
F;66,71/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:D16442; PIDN:BAA03911.1
A;Experimental source: cv. Nipponbare, root
C;Superfamily: peroxidase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;34-109/Disulfide bonds: #status predicted
F;61/Active site: Arg #status predicted
F;65,187/Binding site: heme iron (His) (axial ligands) #status predicted
F;65-72/Disulfide bonds: #status predicted
F;115-310/Disulfide bonds: #status predicted
F;194-219/Disulfide bonds: #status predicted
                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-316 <BUF>
                                                                                                                                                                                                                                                                                       R:Buffard, D.; Breda, C.; van Huystee, R.B.; Asemota, O.; Pierre, M.; Dang Ha, D.B.; Est Proc. Natl. Acad. Sci. U.S.A. 87, 8874-8878, 1990
A;Title: Molecular cloning of complementary DNAs encoding two cationic peroxidases from A;Reference number: A38265; MUID:91062381; PMID:2247460
A;Accession: A38265
                                                                                                                                                                                                                                                                                                                                                                                                                          peroxidase (EC 1.11.1.7) precursor, cationic (clone PNCI) - peanut (Species: Arzchis hypogaea (peanut) C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 04-Mar-2000 C:Accession: A38265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Oryza sativa (rice)
C; Date: 23-Apr-1999 #sequence_revis:
C; Accession: T03929
R; HOri, M.; Sasaki, T.; Minobe, Y.
submitted to the EMBL Data Library,
A; Description: Peroxidase from rice
        F;119-312/Disulfide bonds: #status
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A; Residues: 1-314 <HOR>
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Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: translated from GB/EMBL/DDBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGDGNLAPIDVQTPVRF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASPTLMQCLVAVSLLSCVAHAQLSPTEYASSCPNLQSIVRAAMTQAVASEQRMGASLLRL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSAYYTNLLSNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKMGNISPLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AARDSVVALGGPSWTVLLGRRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDMV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILAL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSVSLMLLVAAAMAS-AASAQLSATFYDTSCPNALSTIKSAVTAAVNSEPRMGASLVRL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSGAHTIGQAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFHDCFVQGCDASVLL-SGQEQNAGPNAGSLRGFNVVDNIKTQVEAICSQTVSCADILAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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59.1%;
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Pred. No. 1.3e-67
2; Mismatches 8:
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C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; pyroglutamic a
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-316/Product: peroxidase 1 #status predicted <MAT>
F;22-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *#status predicted
F;39/Active site: Arg #status predicted
F;59/Active site: Arg #status predicted
F;63-70/Disulfide bonds: #status predicted
F;63-70/Disulfide bonds: #status predicted
F;63-70/Disulfide bonds: #status predicted
F;63-70/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Baga, M.; Chibbar, R.N.; Kartha, K.K. Plant Mol. Biol. 29, 647-662, 1995
A;Title: Molecular cloning and expression a A;Reference number: S61405; MUID:96128008; A;Accession: S61405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peroxidase (EC 1.11.1.7) 1 precursor - wheat C;Species: Triticum aestivum (common wheat) C;Decies: 7-Apr-1996 #sequence_revision 26-Jul-1996 #text_change C;Accession: S61405; S53107
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A; Residues: 1-316 <BAG>
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117 DILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISI.FGRQGLS
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                                                                                 61 LFFHDCFVQGCDGSILL-DAG---GEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCA 116
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                                                                                                                                                                                                                                                             Similarity 58.
85; Conservative
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58.48;
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                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                             Score 915.5;
Pred. No. 9.5e
41; Mismatches
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Pred. No. 2.3e-67;
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                                                                                                                                                                                                                                                                                          .5e-67;
                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                           Length 316;
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C; Genetics:

A; Introns: 703; 134/3

A; Introns: 703; 134/3

C; Superfamily: peroxidase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F; 24-3/Domain: signal sequence *status predicted <ANIP
F; 24-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form
F; 34-114/Disulfide bonds: *status predicted
F; 61/Active site: Arg *status predicted
F; 61/Active site: Arg *status predicted
F; 61/72/Disulfide bonds: *status predicted
F; 199-224/Disulfide bonds: *status predicted
F; 199-224/Disulfide bonds: *status predicted
F; 199-224/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peroxidase (EC 1.11.1.7) 4 precursor - wheat c;Species: Triticum aestivum (common wheat) C;pate: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 0. C;Accession: S61408; S53110 R;Baga, M.; Chibbar, R.N.; Kartha, K.K. Plant Mol. Biol. 29, 647-662, 1995 A;Title: Molecular cloning and expression analysis of peroxidase A;Reference number: S61405; MUID:96128008; PMID:8541492 A;Accession: S61408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-319 <BAG>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                HDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADIL 119
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                                                                                                                         RFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVL 297
                                                                                                                                                                                   MVALSGAHTIGQAQCQNFRDRLYNETNIDTAFATSLRANCPRPTGSGDSSLAPLDTTTPN
                                                                                                                                                                                                                                                                         HDCFVQGCDASILLSDTATFTGEQGAGPNAGSIRGMNVIDNIKAQVEAVCTQTVSCADIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MQCLVAVSLLSCVA---HAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFF 63
                                                          TGTAGQIRRNCRVVN 312
                                                                                                  AFDNAYYRNLMSQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRDFRAAMVSMGNISPL
                 TGTQGQVRLSCSRVN 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%; Score 895.5; DB 57.5%; Pred. No. 4e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
. B56555
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F;71-76/Disulfide bonds: #status predicted
F;124-318/Disulfide bonds: #status predicted
F;203-229/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: Chromoprotein; heme; iron; metalloprotein; F;1-27/Domain: signal sequence *status predicted <SIG>F;38-118/Disulfide bonds: *status predicted F;38-118/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M74103; NID:9170202
A;Experimental source: protoplasts
A;Experimental source: protoplasts
A;Note: sequence extracted from NCBI backbone (NCBIN:118061, NCBIP:118062)
A;Note: sequence extracted from NCBI backbone (NCBIN:118061, NCBIP:118062)
C;Superfamily: peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-322 < CRI>
                                                                                                                                                                    peroxidase (EC 1.11.1.7) 2 precursor - whea c; Species: Triticum aestivum (common what) C; Date: 27-Apr-1996 #sequence_revision 26-JC; Accession: S61406; S53108 R; Baga, M.; Chibbar, R.N.; Kartha, K.K. Plant Mol. Biol. 29, 647-662, 1995
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S61406
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A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-314 <BAS-A; Residues: 1-314 <BAS-A; Residues: 1-314 <BAS-A; RID:g732971; PIDN:CAA59485.1; PID:g7A; Note: exon/intron junctions have been confirmed by mRNA sequencing C; Genetics:
                                                                                                       A; Title: Molecular cloning and expression analysis of peroxidase A; Reference number: S61405; MUID:96128008; PMID:8541492 A; Accession: S61406
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ech. Dev. 38, 121-132,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLIRLHFHDCFVQGCDASILLDETPSIESEKTALPNLGSARGFGIIEDAKREVEKICPG
                                                                                                                                                                                                                                                                                                                                                                                                                                MGNVGVLTGTAGQIRRNCRVVN 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVSCADILTVAARDASAAVGGPSWTVKLGRRDSTTASKTLAETDLPGPFDPLNRLISSFA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASILRLFFHDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGDISPLSGQNGIIRKVCGSVN
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                                            EMBL: x85228; NID: g732971; PIDN: CAA59485.1; PID: g732972
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9; Mismatches
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Pred. No. 5
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. 5.4e-65;
tches 82;
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C;Superfamily: peroxidase
C;Keywords: chromoprotein; glycoprotein; heme; iron; me
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-312/Product: peroxidase #status predicted <MAT>
F;34-107/Disulfide bonds: #status predicted
F;104-Active site: Arg #status predicted
F;65,185/Binding site: heme iron (His) (axial ligands)
F;67-70/Disulfide bonds: #status predicted
F;113-907/Disulfide bonds: #status predicted
F;113-907/Disulfide bonds: #status predicted
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S13325
                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-312 <HER>
                                                                                                                                                                                                                                                                                                                                                                R;Hertly, C.; Rebmann, G.; Bull, J.; Mauch, F.; Dudler, R.
Plant Mol. Biol. 16, 171-174, 1991
A;Title: Sequence and tissue-specific expression of a putative peroxidase gene from whea A;Reference number: S13325; MUID:91363838; PMID:1653627
A;Accession: S13325
                                                                                                                                                                                                                                                                                                                                                                                                                                                               peroxidase (EC 1.11.1.7) precursor - wheat C;Species: Triticum aestivum (common wheat) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                                                                                                                                                                                                                                                          A; Introns: 68/3; 127/3
                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                           A; Cross-references: GB: X53675;
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R;Hertig, C.; Rebman
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C;Superfamily: peroxidase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreduc:
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-314/Product: peroxidase 2 #status predicted <MAT>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature F;34-109/Disulfide bonds: #status predicted
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           Matches 173;
                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCDASVLL-SGMEQNAGPNVGSLRGFGVIDNIKTQLESICKQTVSCADILTVAARDSVVA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVVLVALATAASGQLSSTFYDTSCPRALATIKSGVAAAVSSDPRMGASLLRLHFHDCFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVVNS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOKGLLHSDOVLENNDTTDNTVRNFASNAAAFSSAFTTAMIKMGNIAPLTGTQGQIRLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRNC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKAQCSNFRTRIYGGDTNINTAFATSLKANCPOSGGNTNLENLDTTTPNAFDNAYYTNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGPSWTVPLGRRDSTTASASLANSDLPGPSSSRSQLEAAFLKKNLNTVDMVALSGAHTI
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                           Similarity
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           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.1%; Sco.
56.4%; Pre
                      53.0%;
55.1%;
                                                                                                                                                                                                                                                                                                                                              conceptual translation
                                                                                                                                                                                                                                                                                    GB:S54871; NID:g21830; PIDN:CAA37713.1;
       51;
     Score 849.5;
Pred. No. 2.1e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 8e-63;
                    .le-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                       DB
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                                       ٧,
                                                                                                                                                                                                                metalloprotein; oxidoreductase
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     Indels
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                                       312;
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F:58/Active site: Arg #status predicted
F:62,189/Binding site: heme iron (His) (axial ligands) #status
F:64-69/Disulfide bonds: #status predicted
F:117-311/Disulfide bonds: #status predicted
F:196-221/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Superfamily: peroxidase
C:Keywords: heme; iron; metalloprotein; oxid
F:31-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: T09165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z16599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable peroxidase (EC 1.11.1.7) (clone PC18) - spinach C;Species: Spinacia oleracea (spinach) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_C;Accession: T09165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: prxr5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: subspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type:
A; Residues: 1-31
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Best Local
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252 GLFHSDQELFNGGSQ-DALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRNCRV
                                      194
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                                                     ARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFDTAYFTNLLSRR 251
                                                                                                                        GPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAHTIGQ 191
                                                                                                                                                                                    LLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLG 131
                                                                                                                                                                                                                                    LSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQGCDGSI 75
                                                                                               GPTWQVRLGRRDSLTANRSAANAFIPAPSFNLRNLTSSFTTVGLSFKDMVVLSGAHTVGF 193
                                                                                                                                                                  LLDDTSTFRGEKTAIPNKNSVRGFKAVDSIKASLEKACPGVVSCADILAIASRDAVVQYG 133
                               ARCTSFRPHIHNDTNINAAFAKSLQKKCPQSGNGKVLQPLDYQTKFRFDDKYYQNLLVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNAYYTNLLSQKGLLHSDQVLFNNETTDNTVRNFASNAAAFSSAFTTAMIKMGNIAPLTG
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                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                     52.8%;
56.3%;
                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                       Score 846.5;
Pred. No. 3.7e
42; Mismatches
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                                                                                                                                                                                                                                                                                                                   .7e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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F;64,186/Binding site: heme iron (His) (axial ligands) #status predicted
F;66-71/Disulfide bonds: #status predicted
F;114-307/Disulfide bonds: #status predicted
F;193-218/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Rebmann, G.; Hertig, C.; Bull, J.; Mauch, F.; Dudler, R.

l'ant Mol. Biol. 16, 329-331, 1991

"Title: Cloning and sequencing of cDNAs encoding a pathogen-induced putative peroxidase; Reference number: S13375; MUID:91370874; PMID:1893103

Accession: $13375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: mRNA;Residues: 1-312 <REB>;Residues: 1-312 <REB>;CRESTORES - FID: GB: X55011; GB: X55687; NID: G21828; PIDN: CAA39486.1; PID: G21829;Rote: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 135-Tyr;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 135-Tyr;Superfamily: peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reywords: chromoprotein; glycoprotein; heme; iron; metalloprotein; oxidoreductase 1-22/Domain: signal sequence #status predicted <SIG> 23-312/Product: peroxidase #status predicted <MAT> 33-108/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                             180 VALSGAHTIGQAQCGTFKDRIYNETNIDTAFATSLRANCERSNGDGSLANLDTTTANTED 239
                                                                                                                                                                                                                                                                                                                                                           181 TALSGAHTIGGARCTTERGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQTPVRFD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTTASLGTLISLFGRQGLSPRDM 180
                                                                                                           300 QGQIRLSCSRVNS 312
                                                                                                                                                                 301 AGQIRRNCRVVNS 313
                                                                                                                                                                                                                       240 NAYYTNLMSQKGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                        120 VAARDSVVALGGPSWTVPLGRRDSTDANEAAANSDLPGFTSSRSDLELAFRNKGLLTIDM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAASASCLSLVVLVALATAASAQLSPTFYDTSCPRALAIIKSGVMAAVSSDPRMGASLLR 60
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Maximum Match 100%
Listing first 45 summaries
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p15232 armoracia r
p24101 arabidopsis
p24102 arabidopsis
p17100 armoracia r
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34 101 6.3 372 1 LIGC_TRAVE 35 99 6.2 486 1 CUGL_HUMAN 36 99 6.2 486 1 CUGL_HOUSE 37 97 6.0 517 1 HEX_ADEO8 38 96 6.0 730 1 CATA_HALMA 40 95 5.9 372 1 LIGG_PHACH 41 93 5.8 345 1 THSR_ARCFU 41 93 5.8 545 1 THSR_ARCFU 42 91 5.7 1672 1 PMPB_CHLMU 43 90.5 5.6 349 1 TLY9_ARATH 44 90.5 5.6 1196 1 ICEV_PSESX 45 90 5.6 554 1 ILVD_THEMA	101 6.3 486 1 99 6.2 486 1 99 6.2 486 1 97 6.0 517 1 96 6.0 730 1 95 5.9 372 1 95 5.9 397 1 93 5.8 545 1 90.5 5.6 1196 1 90.5 5.6 1196 554 1
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	P20019 P28659 P28659 P36859 P56622 P50622 P04633 O28045 O99142 O9924721

ALIGNMENTS

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"Amino-acid sequences of heme-linked, histidine-containing peptides of five peroxidases from horseradish and turnip.";

Eur. J. Blochem. 73:353-358(1977).

-i- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + 2 H(2)O(2).

-i- COPACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

-i- MISCELLANEOUS: THE PROTEIN SHOWN, TPJ. IS THE PRINCIPAL ISOPEROXIDASE DURING WINTER IN TURNIP.

-i- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P00434;
P00434;
P1-JUL-1986 (Rel. 01, Created)
21-JUL-1984 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peroxidase P7 (EC 1.11.1.7).
Brassica rapa (Turnip).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Brassica.
NCBL_TaxID-51350;
                                                                                                                                                                                                                                                                                                                                    PIR; A00503; OPNB7.
PIR; B23116; B23116.
HSSP; P22195; ISCH.
InterPro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mazza G., Welinder K.G.;
"Covalent structure of turnip peroxidase 7. Cyanogen bromide fragments, complete structure and comparison to horseradish peroxidase C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 32-65 AND 161-175.
MEDLINE=77138218; PubMed=849740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Blanc dur d'hiver; MEDLINE=81003872; PubMed=7408
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N-LINKED (GLCNAC. . .).
53C9CCE59B2A7937 CRC64;
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BY SIMILARITY
DISTAL HISTIDINE (BY SIMILARITY).
IRON (PROTOHEME IX AXIAL LIGAND).
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Similarity

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Length 296;

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Best Local
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PERL_ARAHY STANDARD,
P22195;
01-NG-1991 (Rel. 19, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
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the Europ
use by
modified
                                                                                                                                                                                                                       Structure 4:311-321(1996).

-1- FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LICHIN, DEFENSE RESPONSE TOWARD WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

-1- CATALYTIC ACTIVITY: Donor + H(2)0(2) = oxidized donor + 2 H(2)0.

-1- COFACTOR: Binds 1 protoheme IX, 1 iron(III) ion and 2 calcium io
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buffard D., Breda C., van Huystee R.B., Asemota Dang Ha D.B., Esnault R.; Dang Ha D.B., Esnault R.; Molecular cloning of complementary DNAs encodin peroxidases from cultivated peanut cells."; Proc. Natl. Acad. Sci. U.S.A. 87:8874-8878(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arachis hypogaea (Peanut).
Eukaryota; Viridiplantae; Strep
Spermatophyta; Magnoliophyta; e
eurosids I; Fabales; Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-91062381; PubMed-2247460;
                                                                                                                                                                                                                                                                                                                                                                                                  Schuller D.J., Ban N., van Huystee R.B., McPhe "The crystal structure of peanut peroxidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTI MEDLINE-96398617; PubMed-8805539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arachis.
                       This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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3.8e-68;
66;
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MOD_RES
CARBOHYD
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GlycoSuiteDB; P22195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00435; PEROXIDASE_1; 1. PROSITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002016; Peroxidase
Pfam; PF00141; peroxidase; 1.
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1SCH; 1
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                                                                        GQIRTNCRKTN
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                                                                                                                                         AYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTA
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58.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISTAL HISTIDINE.
IRON (PROTOHEME IX AXIAL LIGAND).
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
/FTId=CAR_000185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 927; DB 1;
Pred. No. 6.4e-67;
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CATIONIC PEROXIDASE
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15-JUN-2002
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CARBOHYD
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LIGHT, DEFENSE RESPONSE TORP WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
-!- CATALYTIC ACTIVITY: Donor + H(2)0(2) = oxidized donor + 2 H(2) - CATALYTIC BOTOR IN TABLE ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZYME/ISOZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002016; Peroxidase
Pfam; PF00141; peroxidase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peroxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene family;
         182
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                                                                                                                                                                                                                                                                                                          ASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRL
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                                                                                      FFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILAL
                                                                                                                                                                             HFHDCFVQGCDASVLL-SGQEQNAGPNAGSLRGFNVVDNIKTQVEAICSQTVSCADILAV
  ALSGAHTIGOAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAF
                                            ALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPR--SGGDGNLAPIDVQTPVRF
                                                                                                                                                                                                                                                                       ASSVSLMLLVAAAMAS-AASAQLSATFYDTSCPNALSTIKSAVTAAVNSEPRMGASLVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D16442; BAA03911.1; -. P22195; 1SCH.
                                                                                                                                                                                                                                                                                                                                                                     185;
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nipponbare; TISSUE=Root; asaki T., Minobe Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor
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Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30,
30,
41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314
24
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187
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169
203
274
309
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59.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         32606 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PEROXIDASE.

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

DISTAL HISTIDINE (BY SIMILARITY).

IRON (PROTOHEME IX AXIAL LIGAND) (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eptophyta; Embryophyta; Tracheophyta;
Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peroxidase; Iron;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     . 926;
7.
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                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
.6e-67;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 314;
                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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L outstation -
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                MOD_RES
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                                                                                                                                                                                                                                                                                            PROSITE;
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PR00458;

PEROXIDASE. PEROXIDASE_1; PEROXIDASE_2;

PS00436; PS00435;

Peroxidase;

Iron; Heme;

Glycoprotein; Signal.

196 196

65 196

IRON

(PROTOHEME

(BY SIMILARITY).

AXIAL LIGAND)

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28

322 28

LIGNIN FORMING ANIONIC PYRROLIDONE CARBOXYLIC

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PEROXIDASE

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RESULT 4
PERX_NICSY
                                         EMBL; M74103; AAA34050.1; HSSP; P22195; 1SCH.
                                                                                                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                       the
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana sylvestris be replicational activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Criqui M.-C., Pless
Jamet E., Fleck J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93041285;
Criqui M - 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lignin forming anionic peroxidase precursor (EC 1.11. Nicotiana sylvestris (Wood tobacco). Eukaryota; Viridipiantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel.
01-JUL-1993 (Rel.
15-JUN-2002 (Rel.
    Pfam; PF00141;
                                                                                                                                              modified
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Nicotiana sylvestris before
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                       InterPro;
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                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + COFACTOR: Binds I protoheme IX and I iron(III) ion. TISSUE SPECIFICITY: MESOPHYLL PROTOPLASTS AND TO A MUCH EXTENT, ROOTS AND GERMINATING SEEDS.

DEVELOPMENTAL STAGE: BEFORE RE-INITIATION OF THE DNA RELEASED.
                                                                                                                                                                                                                                                                                                                                                                                                                                   h. Dev. 38:121-132(1992).

FUNCTION: THIS ENZYME PLAYS AN INTEGRAL ROLE IN SECONDA WALL BIOSYNTHESIS BY THE POLYMERIZATION OF CINNAMYL ALCINTO LICHN AND BY FORMING RIGID CROSS-LINKS BETWEEN CE PECTIN, HYDROXY-PROLINE-RICH GLYCOPROTEINS, AND LIGNIN.
                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                        SUBFAMILY
                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTAYFTNILLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSAYYTNLLSNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKMGNISPLTG
                                                                                                                    pean Bioinformatics Institute. The non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM
                       IPR002016; Peroxidase.
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peroxidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanaceae;
                                                                                                                         (See http://www.isb-sib.ch/announce/
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Best Local S
Matches 181
                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence upds)
15-JUN-2002 (Rel. 41, Last annotation upd)
Peroxidase precursor (EC 1.11.1.7).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnollophyta; Lillopsid;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHEAT
                      EMBL;
                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             STRAIN-cv. Cheyenne; MEDLINE-91363838; PubMed-1653627;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PER1_WHEAT Q05855;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4565;
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                                                                                                                                                        SIMILARITY: BELONGS
                                                                                                                                              SUBFAMILY.
            S13325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNTPTQSFRAKAAIFSLLLLSCMQCHAQLSATFYDNTCPNALNTIRTSVRQAISSERRMA
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                         x53675;
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213
322
            S13325
                         CAA37713.1;
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213
34646
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56.2%;
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TO THE PEROXIDASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                              Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                     Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OC154F2DC2596449 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                        PLANT PEROXIDASE
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RESULT
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Best Local S
Matches 173
                                                                                                                                                                                             PER1_HORVU STANDARD; PRT; 3
P27337;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Peroxidase 1 precursor (EC 1.11.1.7).
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ACT_SITE
ACT_SITE
Erysiphe graminis.";
Physiol. Mol. Plant Pathol.
-!- FUNCTION: INVOLVED IN DE
                                    SEQUENCE FROM N.A.

STRAIN-CV. Pallas / P-01; TISSUE-Seedling leaf;
Thordal-Christensen H., Brandt J., Cho B.H., Rasmussen S.K.,
Gregersen P.L., Smedegaard-Petersen V., Collinge D.B.;
"CDNA cloning and characterization of two barley peroxidase transcripts induced differentially by the powdery mildew fungus Erysiphe graminis.";
                                                                                                                                                   Hordeum vulgare (Barley).
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Envaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00141; peroxidase; 1. PRINTS; PR00458; PEROXIDASE.1; PROSITE; PS00435; PEROXIDASE_1; PROSITE; PS00436; PEROXIDASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Glycoprotein; Peroxidase; Multigene family; Signal.
                                                                                                                                                  Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                         HORVU
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                                                                                                                                     NCBI_TaxID=4513;
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DISTAL HISTIDINE (BY SIMILARITY).
DISTAL HISTIDINE (IX AXIAL LIGAND) (B SIMILARITY).
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01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, I
15-JUN-2002 (Rel. 41, I
Peroxidase (EC 1.11.1.7)
Armoracia rusticana (Hc
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HSSP; P22195; 1SCH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00435; PEROXIDASE_1; PROSITE; PS00436; PEROXIDASE_2; Oxidoreductase; Glycoprotein; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
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                                                    P80679;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion. SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY
                                                                                                                                                                                                                                                LFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILA
                                                                                                                KTGTQGQIRLSCSRVNS
                                                                                                                                                                   VRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGV
                                                                                                                                                                                              MTALSGAHTIGQARCTTFRGRIY-GDTDINASFAALRQQTCFRS--GGDGNLAPIDVQTP
                                                                                                                                                                                                                                   LHFHDCFVQGCDASVLL-SGMEQNAIPNAGSLRGFGVIDSIKTQIEAICKQTVSCADILT
                                                                                                                                                                                                                                                                                                                    MASSSYTSLLVLVALVT-AASAQLSPTFYDTSCPRALATIKSGVMAAVTSDPRMGASLLR
                                                                                                                                  LTGTAGQIRRNCRVVNS
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                                                                                                                                                                                                                                                                                                                                                            170;
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315 AA;
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PEROXIDASE 1.
BY SIMILARITY.
DISTAL HISTIDINE
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Pred. No.
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                                 update)
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                      update)
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mussen C.B., Stoffer B., Welinder K.G.;
mitted (AUG-1996) to the SWISS-PROT data bank.
FUNCTION: REMOVAL OF H(2)O(2), OXIDATION OF TOXIC REDUCTP
BIOSYNTHESIS AND DEGRADATION OF LIGHIN, DEFENSE RESPONSE
WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT E
DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      _SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS
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                                                                                                                                   LGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAHTIGQARCTTER 198
                                                                                                                                                                             ---EKTAGPNINSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNILGGPTWSVP 138
                                                                                                                                                                                                            QLNATFYSGTCPNASAIVRSTIQQAFQSDTRIGASLIRLHFHDCFVDGCDASILLDDSGS
                    VVN 312
                                        GLLQSDQELFSTLGSATIAVVTSFASNQTLFFQAFAQSMINMGNISPLTGSNGEIRLDCK
                                                  GLFHSDQELFN--GGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRNCR
                                                                                 NRLFNFSGTNGPDPTLNSTLLSSLQQLCPQNGSASTITNLDLSTPDAFDNNYFANLQSNN
                                                                                                                                                                  IQSEKNAGPNANSARGFNYVDNIKTALENTCPGVVSCSDILALASEASVSLTGGPSWTVL
                                                                                                                           LGRRDSLTANLAGANSAIPSPFEGLSNITSKFSAVGLNTNDLVALSGAHTFGRARCGVFN
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PS00436;
 303
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13
147
185
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267
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                                                                                                                                                                                                                                                                                                                                                                                                                                            42
64
169
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Y: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Glycoprotein;
2 42 B
4 64 D
9 169 I
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PEROXIDASE_2;
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BY SIMILARITY.
PYRROLIDONE CARBOXYLIC P
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
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Pred. No. 9.6e
18; Mismatches
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DISTAL HISTIDINE
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ESPONSE TOWARD
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RESULT 8
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PROSITE; PS00436; PEROXIDASE_2; 1.
Ovidoroductase; Peroxidase; Iron; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

NCBI_TaxID-4097;
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
Lignin forming anionic peroxidase precursor
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HSSP; P00433; 2ATJ.
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VPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSGAHTIGQARCTT 196
                                                                                                                                                                SNAQLSATEYDTTCPNVTSIVRGVMDQRQRTDARAGAKIIRLHFHDCFVNGCDGSILLDT
                                                                    DGTQTEKDAPANVGA-GGFDIVDDIKTALENVCPGVVSCADILALASEIGVVLAKGPSWQ 138
                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                   EKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGTNLLGGPTWS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        email to license@isb-sib.ch).
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48.7%;
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PYROKLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
DISTAL HISTIDINE (BY SIMILARITY).
IRON (PROTOHEME IX AXIAL LIGAND) (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                               50;
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Pred. No. 1.2e
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l.2e-50;
nes 93;
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g the lignin-forming
tissue-specific
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PSEQUENCE FROM N.A.

MEDILINE-88225087; PubMed-3371352;

A Fujiyama K., Takemura H., Shibayama S., Kobayashi K., Choi J.K.,

A Fujiyama K., Takemura H., Shibayama S., Kobayashi K., Choi J.K.,

A Shinmyo A., Takemura H., Shibayama S., Kobayashi K., Choi J.K.,

A Shinmyo A., Takemura H., Shibayama S., Kobayashi K., Choi J.K.,

A Shinmyo A., Takemura H., Shibayama S., Kobayashi K., Choi J.K.,

A Shinmyo A., Takenura H., Shibayama S., Kobayashi K., Choi J.K.,

A Shinmyo A., Takenura H., Yanda Y., Okada H.;

T "Structure of the horseradish peroxidase isozyme C genes.";

Eur. J. Biochem. 173:681-687(1988).

C -!- FUNCTION: REMOVAL OF H.(2)0(2), OXIDATION OF TOXIC REDUCTANTS

BIOSYNCHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TOWN

WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE

C -!- CATALYTIC ACTIVITY: DODOT + H(2)0(2) - OXIDATION OF TOXIC REDUCTANTS

C -!- COPACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

C -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE

C -!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
   DISULFID DISULFID
                                                                ACT_SITE
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                                                 METAL
                                                                                                                                                                                                                                                                   EMBL; M60729; AAA33379.1;
PIR; S00627; S00627.
HSSP; P00433; 2ATJ.
                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as low modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peroxidase CIC precursor (EC 1.11.1.7) (Fragment).
                                                                                                                                                                                                                          PROSITE;
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TE; PS00435; PEROXIDASE_1;
TE; PS00436; PEROXIDASE_2;
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                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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PYRROLIDONE CA
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BY SIMILARITY.
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RESULT 10
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Best Local Similarity
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21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation upda
15-JUN-2002 (Rel. 41, Last annotation upda)
                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II. Brassicales; Brassicaceae; Armora
MEDLINE=98069652; PubMed=9406554; Gajhede M., Schuller D.J., Henriksen A., Smit "Crystal structure of horseradish peroxidase Nat. Struct. Biol. 4:1032-1038(1997).
                                                                                                                                 Fujiyama K., Takemura H., Shibayama S., K
Shinmyo A., Takano M., Yamada Y., Okada F
"Structure of the horseradish peroxidase
Eur. J. Biochem. 173:681-687(1988).
                                                                                                                                                                                                                                                           Peroxidase C1A precursor PRXC1A OR HPRC1.
                                                                                          MEDLINE=77068850; PubMed=1001465;
Welinder K.G.;
                                                                                                               SEQUENCE OF 31-338.
                                                                                                                                                                           MEDLINE=88225087; PubMed=3371352;
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=3704;
                                                                                                                                                                                                                                                Armoracia rusticana (Horseradish)
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                                         X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
                                                                                  "Covalent
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                                                                            structure
                                                             72:19-23(1976)
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           Smith A.T., Poulos T.L.;
dase C at 2.15-A resolution.";
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X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

Meno K., White C.G., Smith A.T., Gajhede M.;

Submitted (DEC-1998) to the PDB data bank.

Submitted (DEC-1998) to the PDB data bank.

FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANTS,

BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TOWARD

WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE

BEDENDENT ON BACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

-!- CATALYTIC ACTIVITY: Donor + H(2)0(2) = oxidized donor + 2 H(2)0.

-!- CORACTOR: Binds 1 protoheme IX, 1 iron(III) ion and 2 calcium io
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural interactions between horseradish peroxidase C and the substrate benzhydroxamic acid determined by X-ray crystallography."; Diochemistry 37:8054-8060(1998).
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Henriksen A., Schuller D.J., Meno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0)
                                                                                                                                                   per subunit.
- SUBUNIT: MONOMER.
- SIMILARITY: BELOW
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EMBL; M37156; AAA33377.1; ALT_SEQ. PIR; A00502; OPRHC. PIR; S00625; S00625. PDB; 1ATJ; 04-FEB-98. PDB; 2ATJ; 28-JAN-98. PDB; 3ATJ; 23-DEC-98. PDB; 3ATJ; 23-DEC-98. GlycoSuiteDB; P00433; -InterPro; IPR002016; Perox Pfam; PF00141; peroxidase; PROSITE; PS00435; PEROXIDASE_1; PROSITE; PS00436; PEROXIDASE_2; 6; PEROXIDASE_2; Glycoprotein; Po PEROXIDASE. Signal; Peroxidase 3D-structure. N-LINKED N-LINKED N-LINKED N-LINKED DISTAL HISTIDINE.
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                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           Fujiyama K., Takemura H., Shibayama S., Kobayashi K., Choi J.K., Shinmyo A., Takano M., Yamada Y., Okada H.;

Shinmyo A., Takano M., Yamada Y., Okada H.;

"Structure of the horseradish peroxidase isozyme C genes.";

Eur. J. Biochem. 173:681-687(1988).

-I- FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LICONIN, DEFENDE RESPONSE TOWARD WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEFENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

-I- CATALYTIC ACTIVITY: DONOT + H(2)0(2) - OXIDIZED donor + 2 H(2)0.

-I- COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

-I- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE SUBFAMILY.
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Armoracia rusticana (Horseradish) (Armoracia laphatifolia).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Armoracia.
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CARBOHYD
SEQUENCE
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01-APR-1990 (Rel. 14, Last sequence upd
15-JUN-2002 (Rel. 41, Last annotation u
Peroxidase CIB precursor (EC 1.11.1.7).
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SEQUENCE FROM N.A. MEDLINE=91200671;
                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magonlophyta; edicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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PROSITE; PS00436; PEROXIDASE_2; 1.
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RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B., Conrad A., Hornischer K., Kauer G., Loehnert T. H., Nordsiek G., Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., RA Reichelt J., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D., Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., RA Cooke R., Laudie M., Flores M., Liquori R., Vitale D., RA Monfort A., Argiriou A., Flores M., Liquori R., Vitale D., RA Monfort A., Argiriou A., Flores M., Liquori R., Vitale D., RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J., RA Mayer K.F.X., Walts A., Utterback T., Fijlic Y., Shea T.P., RA Rooney T., Rizzo M., Walts A., Utterback T., Fijlic Y., Shea T.P., RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E., RA Sasamoto S., Kimura T., Idesawa K., Kawashina K., Kishida Y., RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Watanabe A., Yanada M., Yasuda M., Tabata S.,
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-!- FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANT BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TO WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
-!- CATALYTIC ACTIVITY: Donor + H(2)0(2) = oxidized donor + 2:
-!- COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion.
-!- TISSUE SPECIFICITY: ROOTS.
-!- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXII
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EMBL; AL132967; CAB6199
PIR; JU0457; JU0457.
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01-MAR-1992 (Rel. 21, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Basic peroxidase E precursor (EC 1.11.1.7) (C
                                                                                                         Duroux L., Welinder K.G.; "Structural diversity and transcription of Arabidopsis thaliana.";
                                                                                                                                                                                                                                      "Nucleotide sequences of two Arabidopsis thaliana."; Gene 98:237-241(1991).
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Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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Arabidopsis thaliana (Mouse-ear cress).
MEDLINE=20083487;
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Takano M.;
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Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

RIKEN Arabidopsis full length cDNA clones (RAFLS) sequenced by T SSP consortium (Salk/Stanford/PGEC).";

SUBmilted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

C I - FUNCTION: REMOVAL OF H(2)0(2), OXIDATION OF TOXIC REDUCTANTS BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TOW WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.

C I - CATALYTIC ACTIVITY: DONOT + H(2)0(2) = OXIGIZED donor + 2 H(COFACTOR: Binds 1 protoheme IX and 1 iron(III) ion.

C I - TISSUE SPECIFICITY: ROOTS.

C I - SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDA
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
Oxidoreductase; Glycoprotein; Peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D. Fujil C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldbyum T.V Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Benfat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence and analysis of chromosome 2 thaliana.";
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                                                              Similarity
                                                                                                                        Conservative
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                                                                                                                 Signal
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                                        47;
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DISTAL HISTIDINE (BY SIMILARITY IRON (PROTOHEME IX AX)
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BY SIMILARITY.
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N-LINKED (GLCNAC
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RESPONSE TOWARD
MIGHT BE
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RESULT 14
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                             EMBL; D90116; BAA14144.1; -.
PIR; JH0150; JH0150.
HSSP; P00433; ZATJ.
InterPro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
PR.NTS; PR00458; PEROXIDASE_1; 1.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
Oxidoreductase; Glycoprotein; Peroxi
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLING-90323613; PubMed-2373366;
Fujiyama K., Takemura H., Shinmyo
Fujiyama K., Takemura e of two new
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01-AUG-1990
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes."
Gene 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Armoracia rusticana (Horseradish) (Armoracia laphatifolia).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Armoracia.
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P17180;
                Multigene
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BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENSE RESPONSE TOWARD
WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE
DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
CATALYTIC ACTIVITY: Donor + H(2)O(2) = OXIGIZED GONOR + 2 H(2)O.
COPACTOR: Binds 1 protoheme IX and 1 iron(III) ion.
SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEKOXIDASE
SIMPLAMATIVE
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 family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 (Rel. 15, Created)
0 (Rel. 15, Last sequence update)
2 (Rel. 41, Last annotation update)
C3 precursor (EC 1.11.1.7).
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                                    Peroxidase;
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Matches 149;
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P17179;
01-AUG-1990 (Rel. 15, C
01-AUG-1990 (Rel. 15, I
15-JUN-2002 (Rel. 41, I
Peroxidase C2 precursor
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CARBOHYD
                                                                                                                                                    Gene
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache 
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots 
eurosids II; Brassicales; Brassicaceae; Armoracia.
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=90323613; PubMed=2373366;
Fujiyama K., Takemura H., Shinmyo
                                                                                                                                                                                                                                                                                                                                                                                                          PRXC2
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FUNCTION: REMOVAL OF H(2)O(2), OXIDATION OF TOXIC REDUCTANTS, BIOSYNTHESIS AND DEGRADATION OF LIGHN, DEFENSE RESPONSE TOWARD WOUNDING, AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE. CATALYTIC ACTIVITY: DONOT + H(2)O(2) = OXIGIZED donor + 2 H(2)O. COPACTOR: BINDS 1 POTCOHOME IX and 1 ITON(III) ion.

SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. PLANT PEROXIDASE
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Pred. No. 4.3e-47;
7; Mismatches 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                     GCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARD 125
           NVGVLTGTAGQIRRNCRVVNS
                                                                                                  GAHTIGQARCTTFRGRIYG------DTDINASFAALRQQTCPRSGGDGNLAPIDVQTPV
                                                                                                                                           GTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLS-PRDMTALS
NLSPSTGKQGEIRLNCRVVNS
                                        IFDNKYYVNLKENKGLIQSDQELFS-
                                                            RFDTAYFTNLLSRRGLFHSDQELFNGGSQDA----LVRQYSASASLFNADFVAAMIRMG
                                                                                 GGHTFGKNQCQFIMDRLYNFSNSGKPDPTLDKSYLSTLRKQCPRNGNLSVLVDFDLRTPT
                                                                                                                                                                                                                                                  151;
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                                                                                                                                                                                                                                                            Similarity
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N-LINKED (GLCNAC...)
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PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peroxidase;
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L outstation -
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Search completed: April 26, 2003, 12:34:05 Job time: 27 secs

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Q9XGV6
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6 gosspium h
0 spinacia ol
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7 scutellaria
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ALIGNMENTS

Qy 1	Query Match Best Local : Matches 25	SQ SEQUENCE		KW Oxido				DR HSSP;		•			RA ROSS				OC Panio					•	DT 01-NC		ID Q43416	Q43416
MASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLR : :	Query Match Best Local Similarity 81.59 Matches 255; Conservative		L 1	Oxidoreductase; Peroxidase; Signal	DDOGITE: DCOOKSE: DEBOVIDACE	Pfam; PF00141; peroxidase; 1.	InterPro; IPR002016; Peroxidase.	HSSP; P22195; 1SCH.	EMBL; U12314; AAA20472.1;	is (1994), Bo	buffel grass.";	"Investigation of peroxidase	SIXAIN-CV. BIHOELA; TISSOE-WOONDED	SECUENCE FROM N.A.	ance edon n	NCBI_TaxID=35872;	Panicoideae; Paniceae; Cenchrus.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta	Cenchrus ciliaris (Buffelgrass) (Pennisetum ciliare)	v	01-MAR-2002 (TrEM		2		
AASPTLMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRNGASLLI 	80.5%; 81.5%; vative 24	24 307 PEROXIDASE. 307 AA; 32507 MW; 526B44B3A7C75FA7 CRC64;		eroxidase; S	PEROXIDASE.	roxidase; 1.	16; Peroxida:	н.	20472.1;	tany, Univer:	7	peroxidase	A; TISSUE=WO				ceae; Cenchrı	gnoliophyta;	plantae; Str	(Buffelgras	sor (EC 1.11	(TrEMBLiel. 20, Li			PRELIMINARY;	
SPTFYASSCPNL	Score 1292; DB Pred. No. 2e-96; 24; Mismatches	PEROXIDASE. 526B44B3A7	POTENTIAL.	ignal.			se.		•	sity of Quee	90000	and					us.	Liliopsida;	eptophyta; E	s) (Penniset	.1.7).	20, Last annotation update)	01, Created)	•	PRT; 307 AA	
QSIVRAAMTQA :: OTVVRAAMTQA	DB 10; 96; 28;	C75FA7 CRC							ė.	nsland.		netic trans	WOUNDED LEZ					Poales; Po	mbryophyta	um ciliare	•	on update)	1		AA.	
AVASEQRMGASI : : VSSFPRMGASI	Length 307; Indels 6;	54;					(Х	7000			genetic transformation in	AND UNWOUNDED LEAVES, AND STEMS;					oaceae; PACC	Tracheophy			•				
LR 60	Gaps 4;			•				KC-0-200	186	2 × C		3	CEMS;			•		clade;	/ta;		-					

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Best Local S
Matches 221
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Q1.NOV-1999 (TrEMBLrel. 12, Created)
Q1.NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1.MAR-2002 (TrEMBLrel. 20, Last annotation update)
Bacterial-induced peroxidase precursor (EC 1.11.1.7).
Gossypium hirsutum (Upland cotton).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002016; peroxidase.

Pfam; PF00141; peroxidase; 1.

PRINTS; PR00458; PEROXIDASE.

PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.

PROSITE; PS00436; PEROXIDASE_2; 1.

Oxidoreductase; Peroxidase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. REBA B50;
Assigbetse K., Cuny G., Valette C., Delannoy E., Bresson E.,
Jalloul A., Daniel J.-F., Geiger J.-P., Nicole M.;
Tcloning and Characterization of a Bacterial Induced Peroxidase-
"Cloning and Characterization (Accession No. AF155124). (PGR99-129).
Plant Physiol. 121:312-3137(1999).
Plant Physiol. 121:312-3137(1999).
EMBL; AF155124; AAD43561.1;
                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3635;
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180
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STRDLTALSGGHTIGLARCTTFRGRIYNDTNIDANFAATRRANCPASGGDNNLAPLDIQT
                                    SPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDGNLAPIDVQT
                                                                                       ADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGL
                                                                                                                                                RLFFHDCFVNGCDGSILLDDTATFTGEKNAVPNRNSARGFEVIDTIKTNVEAACSATVSC
                                                                                                                                                                 RLFFHDCFVQGCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSC
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                                                                        ADILALAARDGVALLGGPTWQVPLGRRDARTASQSAANNQIPSPFANLATLTSSFAAKGL
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                                                                                                                                                                                                                                                                                                               Similarity
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316 AA;
                                                                                                                                                                                                                                                                                              Conservative
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33696 MW;
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69.7%;
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Pred. No. 8
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BACTERIAL-INDUCED PEROXIDASE
BEB1C05BDEC47F96 CRC64;
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                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. AF155124). (PGR99-129).";
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Query Match
Best Local Similarity
Matches 195; Conserv
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NON_TER 1
SIGNAL <1
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ
EMBL; Y10467; CAA71493.1; -.
HSSP; P22195; ISCH.
InterPro; IPR002016; Peroxidase.
InterPro; IPR000062; Thymidylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spinacia oleracea (Spinach).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00435; PEROXIDASE_1; UNKNO)
PROSITE; PS00436; PEROXIDASE_2; 1.
PROSITE; PS01331; THYMIDYLATE_KINASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00141; peroxidase; 1 PRINTS; PR00458; PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Diveristy and conservation of plant peroxidases."; Plant Peroxidase Newsletter 1:4-7(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                     VLTGTAGQIRRNCRVVN 312
|||| |:||||||||
PLTGTQGEIRRNCRVVN 316
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YKNLIAKRGLLHSDQELYNGGSQDALVTRYSKSNAAFAKDFVAAIIKMGNISPLTGSSGE
                      FTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQ
                                                                                      AHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSG--GDGNLAPIDVQTPVRFDTAY
                                                                                                                                        IILAYLACLSNAQLSSKHYASSCPNLEKIVRKTMKQAVQKEQRMGASILRLFFHDCFVNG
                                                                    GTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGRQGLSPRDMTALSG
                                                                                                                                                                                                              CDASLLLDDTSTFTGEKTAISNRNNSVRGFEVIDSIKTNVEASCKATVSCADILALAARD
                                                                                                                                                                                                                                                                                                                                                                                                                              309
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(TIEMBLIEL 03, Last sequence upda
(TIEMBLIEL 20, Last annotation up
precursor (EC 1.11.1.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peroxidase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                               309
                                                                                                                                                                                                                                                                                                                                                                                                                            33452 MW;
                                                                                                                                                                                                                                                                                                                                                                       62.6%;
                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                         Score 1004.5;
Pred. No. 3.36
                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
; C6D54D73E1390755 CRC64;
                                                                                                                                                                                                                                                                                                                                                     ore 1004.5; DB 10;
ed. No. 3.3e-73;
Mismatches 61; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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QY

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IRRNCRVVN

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DT 0:
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Best Local S
Matches 197
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InterPro; IPR002016; Peroxidase. Pfam; PF00141; Peroxidase; 1. PRINTS; PR00458; PEROXIDASE_1; UN PROSITE; PS00435; PEROXIDASE_1; UN PROSITE; PS00436; PEROXIDASE_2; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids I; Majpighiales; Linaceae; Linum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Peroxidase FLXPER4 (EC 1.11.1.7) (Fragment)
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. STORMONT
Omann F., Tyson H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eurosids I; Malp
NCBI_TaxID=4006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00435; PEROXIDASE_1; PROSITE; PS00436; PEROXIDASE_2; Oxidoreductase; Peroxidase.
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                                                                  Q9LWM9;
                                                                                       Q9LWM9
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TRAIN=CV. STORMONT CIRRUS; TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                             182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDGT 127
                                                                                                                                                                                                CRRPN
                                                                                                                                                                                                                                          CRVVN
                                                                                                                                                                                                                                                                                     LSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRN
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197; Conserv
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) (TrEMBLrel.
) (TrEMBLrel.
? (TrEMBLrel.
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                                                                                         PRELIMINARY;
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15,
21,
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EMBL/GenBank/DDBJ
  Created)
Last sequence
Last annotation
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Pred. No. 1.2e
37; Mismatches
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    update)
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Best Local Similarity
Matches 192; Conserv
                   SEQUENCE FROM N.A. STRAIN=COLUMBIA; MEDLINE=98344145; F Kaneko T., Kotani H Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0451C06.";
Submitted (MAR-2000) to the EMBL/GenBa
EMBL; AP001551; BAA92967.1; -.
HSSP; P22195; ISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
PROSITE; PS00436; PEROXIDASE_2; 1.
SEQUENCE 319 AA; 33536 MW; 395E1BE20BH
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Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. NIPPONBARE;
                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002016; Peroxidase.
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                                                                                                                                                                                                Q9FLC0;
                                                                                   NCBI_TaxID=3702;
                                                                                                                                           AT5G05340
                                                                                                                                                     Peroxidase (Putative peroxidase)
                                                                                                                                                                                                           Q9FLC0
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"Structural analysis of Arabidopsis thaliana chromosome features of the regions of 1,381,565 bp covered by twent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALAVVFLAAEAQLSPGYYNATCPGVVSIVRRGMAQAVQKESRMGASILRLFFHDCFVNG
                                                                                                                                                                                                                                                                                                        TNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLFGROGLSPRDMTALSGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                         GQIRRNCRVVNS
                                                                                                                                                                                                                                                                 GEVRINCRRVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                           PRELIMINARY;
                                PubMed=9679202;
H., Nakamura Y.,
                                                                                                                                                                                                                                                                 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.3%;
61.5%;
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Pred.
                                                                                                                                                                                                            PRT;
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No. 2e
                                  Sato
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                                   Asamizu
                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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   osome 5.
                                   (F)
                                   Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                              Rosidae;
              Sequence
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and TAC

clones

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RESULT
P93548
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Best Local Sim
Matches 199;
                                                                PRXR4.

Spinacia oleracea (Spinach).

Spinacia oleracea (Spinach).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo

Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Chenopodiaceae; Spinacia.
                                                                                                                                               P93548; PRELIMINARY; PRT; 323 AA. P93548; O1-MAY-1997 (TrEMBLrel. 03, Created) O1-MAY-1997 (TrEMBLrel. 03, Last sequence update) O1-MAR-2002 (TrEMBLrel. 20, Last annotation update) Peroxidase precursor (EC 1.11.1.7).
                   Simon P.;
                               TISSUE-LEAF;
                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theologis A.;
Full Length cDNA of gene At5g05340 (GI:15239075).";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ database
EMBL; AB010692; BAB09977.1;
EMBL; AY065270; AAL38746.1;
HSSP; P22195; ISCH.
InterPro; IPRO02016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Shinozaki K., Davis R.W., Soldsn (Schuence From N.A.) Chang C.H., Chang E., Dale J.M., Goldsn (Yamada K., Banh J., Chang C.H., Tang C., Toriumi M., Wi Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H. Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neu Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Nguyen M., Palm C.J., Sakurai T., Satou M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.
  "Diveristy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1;
PROSITE; PS00436; PEROXIDASE_2;
PEROXIDASE_2;
PEROXIDASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physically assigned P1 an
DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                                                                                                                                                             GROGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRS--GGDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASPTLMQCLVAVSLL-----SCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRM
                                                                                                                                                                                                                                                                                                                                                                      APIDVQTPVRFDTAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAM
                                                                                                                                                                                                                                                                                                                                                                                                           SAVGLSTROMVALSGAHTIGQSRCTNFRARIYNETNINAAFATTRQRTCPRASGSGDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVSCADILAIAARDSVVALGGPNWNVKVGRRDARTASQAAANSNIPAPTSSLSQLISSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GASLLRLFFHDCFVQGCDGSILLD----AGGEKTAGDNLNSVRGFEVIDTIKRNVEAACP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASNKLISILVLVVTLLLQGDNNYVVEAQLTTNFYSTSCPNLLSTVQTAVKSAVNSEARM
                                                                                                                                                                                                                                                                                                   IKMGDISPLTGSSGEIRKVCGRTN
                                                                                                                                                                                                                                                                                                                              IRMGNVGVLTGTAGQIRRNCRVVN
                                                                                                                                                                                                                                                                                                                                                       APLDYTTAASFDNNYFKNLMTQRGLLHSDQVLFNGGSTDSIVRGYSNNPSSFNSDFTAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
 conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.1%; Score 980; 61.4%; Pred. No. 3.
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plant
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peroxidases.";
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Carninci P., Chen H., Cheuk R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
3.3e-71;
nes 77;
                                                                                                                                                                    update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                           Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldsmith A.D.,
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RESULT
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STRAIN=CY. SAMSUN NN; TISSUB=TMV-INFECTED LEAF;
STRAIN=CY. SAMSUN NN; TISSUB=TMV-INFECTED LEAF;
MEDLINE=99418329; PubMed=10490396;
Hiraga S., Ito H., Matsui H., Honma M., Ohashi Y.;
"CONA Sequences for two novel tobacco peroxidase is:
Nos. AB027752 and AB027753; (PGR99-109).";
Plant Physiol. 120:1205-1205(1999).
EMBL; AB027752; BAA82306.1; -.
PARTIES AB027752; BAA82306.1; -.
HSSP; P22195; ISCH
InterPro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 197
                                                                                                                                                                                Q9XIV9;
Q1.NOV-1999 (TrEMBLrel. 12, Created)
Q1.NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1.NOV-1999 (TrEMBLrel. 19, Last annotation update)
Q1.DEC-2001 (TrEMBLrel. 19, Last annotation update)
Peroxidase (EC 1.11.1.7).
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; euasterids I; Solanales; Solanaceae; Nicot
                                                                                                                                                                         NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002016; Peroxidase, Pfam; PF00141; peroxidase; 1. PRINTS; PR00458; PEROXIDASE, PROSITE; PS00458; PEROXIDASE_1; UN PROSITE; PS00436; PEROXIDASE_2; 1. Oxidoreductase; Peroxidase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1997) to t
EMBL; Y10465; CAA71491.1;
HSSP; P22195; ISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                        RMGNVGVLTGTAGQIRRNCRVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RONLNIREMTALSGGHTIGFARCTNFRDHIYNDSNIDPNFAATRKASCPRPTGTGDFNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROGLSPRDMTALSGAHTIGQARCTTFRGRIYGDTDINASFAALRQQTCPRSGGDG--NLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVSCADILALAARDGTNLLGGPTWSVPLGRRDSTTASASLANSNPPPPTASLGTLISLEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLLRLFFHDCFVQGCDGSILLD----AGGEKTAGPNL-NSVRGFEVIDTIKRNVEAACPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASNLVVGFLAIFSIILLLAGTSDAWLRKPHFYASSCPNVEQIVFNTMKQAVSKEPRMGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SILRLFFHDCFVNGCDGSVLLDDTPTSQGEKMAFPNRNNSIRGFEVIDAIKSNVEAACSG
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197; Conserv
PR00458;
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323 ÅA;
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1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 972.5;
Pred. No. 1.:
                                                                                                                                                                                                                                                                                                                                                                                323
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; 8547E125CD56E75E CRC64;
                                                                                                                                                                                                                                                                                                             PRT;
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76;
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                                                                                        isoenzymes
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                                                                                                                                                                                               eudicots;
                                                                                                                                                                                                              Tracheophyta;
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Matches
                                                                                Query Match
Best Local
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                "Identification and molecular characterization of novel peroxidase with structural protein-like properties.";
J. Biol. Chem. 274:26192-26198(1999).
EMBL; AB02449; BAA77389.1; -.
INSEP: P22195; 1SCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
Oxidoreductase; Peroxidase.
SEQUENCE 321 AA; 34369 MW; 9263872E0F92D448 CRC64;
                                                                                                             PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
SEQUENCE 318 AA; 33903 MW; 6CD
                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=99403061; PubMed=10473572;
                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; euasterids I; Lamiales; Lamiaceae; Scutelharia
                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                   Q9SSZ7
                                                                                                                                                                                                                                                                NCBI_TaxID=65409;
                                                                                                                                                                                                                                                                                                       Scutellaria
                                                                                                                                                                                                                                                                                                                   Peroxidase 3
                                                                                                                                             PRINTS;
                                                                                                                                                              InterPro; IPR002016; Peroxidase.
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                             LMLVLLLIGVSNAQLSANFYNTTCPNLLTIIRNAVNSAVSSDTRMGASLLRLHEHDCFVN
                                       LVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGASLLRLFFHDCFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        IRRNCRVVN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTIGQARCTTFRGRIYGDT-DINASFAALRQQTCPRS--GGDGNLAPIDVQTPVRFDTAY
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          GCDGSILLD----AGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCADILALAARD 125
                                                                                                                                                                                                                                                                                                                                                                                                                      IRKNCRRLN 321
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                                                                                                                                           PF00141; peroxidase;
S; PR00458; PEROXIDAS;
                                                                               Similarity
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                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                            PEROXIDASE.
                                                                               59.28;
59.98;
61.5%;
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13,
19,
                                                                     44;
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                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                   Score 950; DB 10;
Pred. No. 8.4e-69;
4; Mismatches 75,
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                                                                                                             6CDD0DA3FE470C83 CRC64;
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                                                                     75;
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RESULT 10
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Best Local
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PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
SEQUENCE 311 AA; 32461 MW; 11E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-CV. IRBBLO; TISSUE-LEAF;
Hilaire E., Young S.A., Willard L.H., McGee J.D., Sweat T.A.
Chittoor J.M., Guikema J.A., Leach J.E.;
"Induction of peroxidase gene POCI during the incompatible of rice with Xanthomonas oryzae pv. oryzae.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF247700; AAF65464.2; -.
HSSP, P2135; ISCH.
InterPro; IPR002016; Peroxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
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               TAYFTNLLSRRGLFHSDQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGT
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59.7%;
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Pred. No. 1.
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024336;
01-JAN-1998
01-JAN-1998
01-MAR-2002
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Q43006;
01-NOV-1996
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Raphanus.
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PROSITE; PS00436; PEROXIDASE_2; 1.
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STRAIN-CV. HANDSOME HALL;
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AA; 33558 MW;
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Last annotation update)
(EC 1.11.1.7)
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Pred. No. 1.
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Best Local
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01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotatic
Cationic peroxidase.
Stylosanthes humilis (Townsville stylo).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; eudicotyledc
eurosids I; Fabales; Fabaceae; Papilionoti
Stylosanthes.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peroxidase precursor (EC 1.11.1.7).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complementary DNA cloning and sequencing putative peroxidase from rice."; Plant Physiol. 100:1611-1612(1992). EMBL; X66125; CAA46916.1; ". HSSP; P22195; ISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation updat Peroxidase precursor (EC 1.11.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. NOHRIN;
Reimmann C., Ringli C.,
                                                     SEQUENCE FROM N.A.
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                                    STRAIN-PATERSON; TISSUE-LEAF
                                                                                      NCBI_TaxID=35628;
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317 AA;
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
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25 POTENTIAL.
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317 P
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Last sequence update)
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; CEC727D0DA30E311 CRC64;
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Pred. No. 5e~67;
                                                                                                                        eptophyta; Embryophyta; Tracheophyta;
eudicotyledons; core eudicots; Rosidae;
; Papillonoideae; Aeschynomeneae;
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poales; Poaceae;
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Best Local :
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01-JAN-1998
01-DEC-2001
                                                                                        MEDLINE-97449844; PubMed-9304860;
Chittoor J.M., Leach J.E., white F.F.;
Chitfoor J.M., Leach J.E., white F.F.;
Induction of a peroxidase gene for item of a peroxidase gene for item by xanthomonas oryzae pv. oryzae.";
Mol. Plant Microbe Interact. 10:861-871(1997).
                                                                                                                                                                                                           Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida
Ehrhartoideae; Oryzeae; Oryza.
Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1;
PROSITE; PS00436; PEROXIDASE_2;
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EMBL; L37790; AABO2554.1; -.
HSSP; P22195; ISCH.
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"Nucleotide sequence of a cationic peroxidase gene forage legume Stylosanthes humilis.";
                                                                EMBL; AF014470; AAC49821.1;
HSSP; P22195; 1SCH.
                                                                                                                                                                       SEQUENCE FROM N.A.
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PRINTS; PR00458; PEROXIDASE
                                                      InterPro; IPR002016; Peroxidase.
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Pred. No. 1.1e-66;
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Best Local
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01-JAN-1998
01-DEC-2001
                                                                                                                                                    Pram; Pr00141; peroxidase; 1.
Pram; Pr001458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE_1;
PROSITE; PS00436; PEROXIDASE_2;
SEQUENCE 317 AA; 32863 MW;
                                                                                                                                                                                                                                 STRAIN-TRBB10; TISSUE-LEAF;
MEDLINE-97449844; PubMed-9304860;
Chittoor J.M., Leach J.E., White F.F.;
PDifferential induction of a peroxidase gene family during infection of rice by Xanthomonas oryzee pv. oryzee.";
Mol. Plant Microbe Interact. 10:861-871(1997).
EMBL; AR014467; AAA49818.1; -.
HSSP; P22195; 1SCH.
                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Snermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceze;
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                                                                  1 MASPT---LMQCLVAVSLLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVASEQRMGAS
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LLRLHFHDCFVQGCDASVLL-SGQEQNAGPNVGSLRGFSVIDNAKARVEAICNQTVSCAD
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                          LLRLFFHDCFVQGCDGSILLDAGGEKTAGPNLNSVRGFEVIDTIKRNVEAACPGVVSCAD 117
                                                   MASATNSSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITAAVNSEARMGAS
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Last sequence update)
Last annotation update)
                                                                                                      Score 919; DB 10;
Pred. No. 2.7e-66;
4; Mismatches 83
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool/US10047825/runat_26042003_111958_7132/app_query.fasta_1.455
-O-/cgn2_1/USPTO_spool/US10047825/runat_26042003_111958_7132/app_query.fasta_1.455
-DB=GenEmbl -QFMT-fastap -SUFFIX=-ge -MINMANCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=200000000
-USER-US10047825_cCGN_1_1_1887_@runat_26042003_111958_7132 -NCPU=6 -ICPU=3
-NO_XUPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_lnv:*
32: em_htg_other:*
33: em_htg_pin:*
34: em_htg_pin:*
35: em_htg_mam:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
40: em_htgo_hum:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Query Query Score Match Length DB ID Description

Result No.

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AF003/3/ Olyza sat L3603 Barley pero AF014470 Oryza sat AX412623 Sequence AX117238 Arabidops AJ286345 Arabidops AF452384 Arabidops AY074296 Arabidops	S. olera S. olera 35 Striga Wheat ml 91 Oryza 34 Striga 17 Oryza 27 Horden 98 Sequen Bailey n	ABU24439 Scutellar L36110 Stylosanthe AF247700 Oryza sat X66125 O.sativa mR M37635 Arachis hyp D16442 Oryza sativ AF0014467 Oryza sat AF014467 Oryza sat AF017034 Zea mays M74103 Nicotiana s AF014469 Oryza sat U12315 Cenchrus ci AF14°278 Phaseolus AF014'468 Oryza sat AF085030 Arabidops AB024438 Scutellar L24170 Linum uisita	Ul2314 Cenchrus ci AF155124 Gossypium AF155124 Gossypium AP005613 Oryza sat AP004731 Oryza sat Y10467 S.oleracea AF049881 Linum usi AY065270 Arabidops Y10465 S.oleracea AB027752 Nicotiana

ALIGNMENTS

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KEYWORDS
SOURCE
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Direct Submission
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Thesis (1994) Botany,
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                                                                                                                                                                                                                                                                                                           /product="peroxidase"
982. .1335
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                                                                                                                                                                                                                                                                                 /note="39
440 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Cenchrus ciliaris"
/cultivar="Biloela"
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127. .9
                                                                                                                                                                                                                                                                                                                                                                                   FNSDFVAAMIKMGNIGANAGQVRRNCRVVNS"
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/db_xref="GI:520568"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="expressed in leaves
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Lucia, Brisbane, Queensland,
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2 Assigbetse,K., Cuny,G., Valette,C., Delannoy,E., Bre Assigbetse,K., Cuny,G., Valette,C., Delannoy,E., Bre Assigbetse,K., Cuny,G., Valette,C., Delannoy,E., Bre Assigbetse, C., Delannoy,E., Bre Assigbetse
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Spermatophyta; Magnoliophyta; eudicotyledons; core ex
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium
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                                                                                                                                                                                                                                                                                                                                                                                           /note="disulfide bond" 687. .689
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PSPFANLATLTSSFAAKGLSTRDLTALSGGHTIGLARCTFRGRIYNDTNIDANFAAT
RRANCPASGGDNNLAPLDIQTFTREDNDYFRNLVARRGLLHSDQELFNGGSQDALVRT
YSNNPATFSADFAAAMVKMGNISPLTGTQGEIRRNCRVVN"
                                                                                                                                                                                                                                                                                                                                      /note="proximal histidine; order(708. .710,783. .785) /note="disulfide bond" 735. .737
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/cultivar="Reba B50"
/db_xref="taxon:3635"
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/evidence=not_experimental
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order(312...314,327...329)
/note="disulfide bond"
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order(213. .215,453. .455)
/note="disulfide bond"
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183. .185
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183. .1064
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oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Enspermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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HTG; HTGS_PHASE2.
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NOTE: It currently consists of 1 contigs Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced.
ThrTrpSerValProLeuGlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsn 153
                       TGTTCGAATTGATTCCATAGATTCTGACGGCGACGCGCGTACGTGCAGCTCGGCGGGCCA
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Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7444, Fax:81-298-38-7469)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a 'working draft' segmence.
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Oryza sativa nipponbare(GA3) genomic DN
clone:P0599C12
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                           NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                               Submitted (13-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondal 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tsasaki@nlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel.81-298-38-7441, Fax:81-298-38-7468)
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Sasaki,T., Matsumoto,T.
Direct Submission
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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OSJNBA0016D02, *** SEQUENCING IN PROGRESS
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Query Match: DB:

BASE COUNT ORIGIN Alignment

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US-10-047-825-4 (1-313) x AP004731 (1-158456)
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Best Local Similarity:
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  LeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGly
                                                                                                              ThrAlaSerAlaSerLeuAlaAsnSerAsnProProProProThrAlaSerLeuGlyThr
                                                                                                                                                    TTTGGTGTGCAGCTGGGTGGGCCAACGTGGAGCGTGGCGCTGGGGGCGGAAGGACTCGCGC
                                                                                                                                                                                                                            TGACACGTACGTGAAACCACCCGTACGTCACTGAAATTTTACCAGTGGCTGACATGTTCT
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                                                                                                                                                                                                                                                                                                                                                                               ATCGACGCCATCAAGACGCAGGTGGAGGCCTCCTGCAAGGCCACCGTCTCCTGCGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AlaGlyGlyGluLysThrAlaGlyProAssLeuAsnSerValAryGlyPheGluVal
ACGTTCACCGGCGAAAGACGACCGGCCCGAACCCCGGGCTCGAGGTG
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cultivar="Nipponbare" 
/db_xref="taxon:39947" 
/chromosome="6" 
/clone="0SJNBa0016D02" 
/35607 c 35786 g 42641 t 239
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                   Simon,P.
Direct Submission
Direct Submission
Submitted (10-JAN-1997) P. Simon, University of Geneva, Lab. Plant
Submitted (10-JAN-1997) P. Simon, University of Geneva, Lab. Plant
Blochemistry and Physiology, Uni-Bastions, Place de Luniversite 3,
Blochemistry and Physiology, Uni-Bastions, Place de Luniversite 3,
CH-1211 Geneva 4, SWITZERLAND
CH-1211 Geneva 4, SWITZERLAND
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Spinacia oleracea.
Spinacia oleracea.
Spinacia oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
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S.oleracea mRNA for peroxidase,
Y10467
Y10467,1 GI:1781331
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/product="peroxidase"
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/db_xref="GI:1781332"
                                                      /codon_start=1
/evidence=experimental
                                                                                              /gene="prxr6"
/EC_number="1.11.1.7"
                                                                                                                                                                                                          /tissue_type="cotyledons"
/clone_lib="lambda UNIZAP-XR/SOC1"
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/tissue_type="stems"
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/db_xref="taxon:3562"
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                                                                                                                                                                                                                                                                                                         /clone="PC23"
                                                                                                                                                                                                                                                                                                                                                             /organism="Spinacia
                                                                                                                                                                                        dev_stage="four-weeks-old"
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                                                                                  AspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGly-----
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                                                                                                                            GCCCACACCATCGGCTTAGCACGTTGTGTAAGCTTCCGACACCATATCTACAACGATACT
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/product="peroxidase flxper4"
/prodeln_id="AAC05277.1"
/proteln_id="AAC05277.1"
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/cultivar="Stormont Cirrus"
/db_xref="taxon:4006"
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/EC_number="1.11.1.7"
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Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.J., Toriumi, M., Yu, G., Bowser, L. Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishda, J., Lam, B., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Kim, C., Lam, B., J., Miranda, M., Narusaka, M., Nayuen, M., Palm, C.J., Sakurai, T., Torium, M., Palm, C.J., Sakurai, T., Tor
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Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Full Length cDNA Clones
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(FLC-1) as a BanHI/XhoI insert.
ecotype: Columbia"
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2 (bases 1 to 1238)

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Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.I., Tang, C.C.,

Gorlumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin Neumann, G., Kawai, J., Kin, C., Lam, B.

Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.,

Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,

Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Lam, B.,

Submitted (03-DEC-2001) Plant Gene Expression Center, 800 Buc Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out t collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishi Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K. 800 Buchanan Ishida, J., the

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Condera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally Theologis, A. (SSP

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               LeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPheValAlaAlaMet
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1 (bases 1 to 1176)
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                                   CysAspGlySerIleLeuLeuAsp-----
                                                                                  AAATCTTGTCCTAAACTTTATCAAACTGTGAAATCAGCAGTGCAATCTGCTATTAACAAG
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--AlaGlyGlyGluLysThrAlaGly

Indels: Gaps: Mismatches:

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Submitted (20-MAY-1999) Hiroyuki Ito, Hokkaido University, Department of Applied Bioscience, Graduate School of Agriculture; Kita-9, Nishi-9, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail:otihechem.agr.hokudai.ac.jp, Tel:81-11-706-2500, Fax:81-11-706-3635)
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Hiraga,S., Ito,H., Matsui,H., Honma,M. and Ohashi,Y.

CDNA sequences for two novel tobacco peroxidase isoenzymes
(Accession Nos. AB027752 and AB027753). (PGR99-109)

Plant Physiol. 120, 1205 (1999)

2 (bases 1 to 1356)
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                                                                                                                                                                                                                             AVQSAINKETRMGASLLRLFFHDCFVNGCDGSLLLDDTSSFTGEKRAAPNVNSARGFE
VIDNIKSAVEKVCPGVVSCADILAVTAADSVVILGGPWNVKLRRDSRTASQSAANS
GIPPATSNLNRLISSFSAVGLSTKDMVALSGALTUGGPKNAVKLVSFRARIYNETNNLDASF
ARTRQSNCPRSSGSGDNNLAPLDLQTPNKFDNNYFKNLVDKKGLLHSDQQLFNGGSAD
SIVTSYSNNPSSFSSDFVTAMIKMGDIRPLTGSNGEIRKNCRRLN*
257 c 266 g 457 t
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/db_xref="Gi:5381253"
/translation="MASLKINAIVLFILVSLLIGSSSAQLSTGFYSKSCPKLYQTVKS
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/clone_lib="lambda gt10"
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/cultivar="Samsun NN"
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                                                                                   Scutellaria baicalensis AB024439
                                       J. Biol. Chem. 99403061
                                              Identification and molecular characterization with structural protein-like properties J. Biol. Chem. 274 (37), 26192-26198 (1999)
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                    Morimoto, S.
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{\tt AspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGlyAsp}
                                                                                                                        AlaHisThrIleGlyGlnAlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
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/db_xref="GI:4760704"
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                  ThrPheTyrAlaSerSerCysProAsnLeuGlnSerIleValArgAlaAlaMetThrGln
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/db_xref="taxon:35628"
/clone="Shpx6"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 1330)
1 (bases 1, Young,S.A., Willard,L.H., McGee,J.D., Sweat,T. Chittoor,J.M., Gulkema,J.A. and Leach,J.E.
Induction of peroxidase gene POC1 during the incompatible
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incompatible strain of Xanthomonas oryzae pv. oryzae"
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O.sativa
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                                                                                                                                                                         Reimmann,C., Ringli,C. and Dudler,R. Complementary DNA cloning and sequencing
                                                                                                                                                                                                                                 Submitted (07-JUN-1992) University of Zuerich, &
                                                                                                                                                                                                                                                                Direct Submission
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzaae; Oryza.
1 (bases 1 to 1287)
                                                                                                                                                                                                                                                                                                                                                                peroxidase.
Oryza sativa.
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                                                                                   /organism="Oryza sativa"
/cultivar="Nohrin"
                                                                                                                Location/Qualifiers
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/codon_start=1
                                          /clone_lib="lambda ZAP
                                                         /clone="pPIR3"
                                                                       /db_xref="taxon:4530"
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               /EC_number="1.11.1.7"
                                                                                                                                                                                                                                 C. Reimmann, Institute for Plant Biology, Zollikerstrasse 107, CH-8008 Zuerich,
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                                                                                                                                                                                                                                                             ACCGACATGGTTGCTCTCTCAGGAGCACACACGATCGGGCAGGCGCAGTGCCAGAATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aeschynomeneae; Arachis.

1 (bases 1 to 1116)
Buffard,D., Breda,C., van Huystee,R.B., Asemota,O., Pierre,M.,
Ha,D.B. and Esnault,R.
Molecular cloning of complementary DNAs encoding two cationic peroxidases from cultivated peanut cells
Proc. Natl. Acad. Sci. U.S.A. 87 (22), 8874-8878 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cationic peroxidase.
Arachis hypogaea cDNA
Arachis hypogaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-AUG-1990) Robert Esnault, Institut des Sciences Vegetales, CNRS, 91198 Gif Sur Yvette, France On Aug 15, 1996 this sequence version replaced gi:166472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arachis hypogaea
M37636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Esnault, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M37636.1 GI:1491775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Rosidae; eurosids I; Fabales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARCPNC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 1116)
                                                                                                                          349
                                                                                                                       LQANCPSVGGDTNLSPFDVTTPNKFDNAYYINLRNKKGLLHSDQQLFNGVSTDSQVTA
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13. .963
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/db_xref="GI:1491776"
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/db_xref="taxon:3818"
/clone="prxPNC1"
                                                                                                                                                                                                                                                                                                                    /gene="PNC1"
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58.52%
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Length:
Matches:
Conservative:
Mismatches:
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		12 60	ValAsn 3 ACCAAC 9	JASnCysArgVal CAATTGCAGGAAG	lnIleArgArgA CAAATTAGAACCA	302 GlyGl 928 GGCCA	Qу
30 92	alLeuThrGlyThrAla ::: CACTCACTGGGACTAGT	alGlyV; ;; fTAGTC	gMetGlyAsnVa : GATGGGAAACC	lAlaAlaMetIleArgMet ::: CAATGCAATGATTAAGATG	PheVa	282 AlaAsp 868 ACTGAC	Qy
86	erAlaSerLeuPheAsn :: ::: ATGCTGCAACTTTCAAC	erAlas 	lArgGlnTyr; CACTGCTTAT	spAlaLeuValArç ::: hTTCCCAAGTCACT	yGlySerGlnAs 	2 AsnGl	Db Qy
80	erAspGlnGluLeuPhe TGATCAACAACTCTTC	uPheHisSe CTTGCATTC	ArgArgGlyLeuPheHisSerAspGlnG :::::: :AGAAGGGTCTCTTGCATTCTGATCAAC	er AC	/rPheThrAsnLeuLeus ::: CTATATCAACTTGAGA/	242 AlaTy 748 GCTTA	Db Qy
241 747	COValArgPheAspThr ::: CAAACAAATTTGACAAT	lGlnThrPr AACAACACC	OIleAspVa ATTTGATGT	pGlyAsnLeuAlaProIleAspValGlnThrProVal. ::: raccaarTTGTCACCATTTGATGTAACAACACCAAAC	erGlyGlyAspGlyA raggaggagatacca	222 SerGl: 688 GTAGG	ОУ
221	InGlnThrCysProArg	aAlaLeuArgGlnGlnT 	heAl:: :: ATGC	anAlaSe :: :: ATCCAAC	rGlyAspThrAspIleAs ::::::: : CAATGAGAGCAACATAGJ	202 TyrGl: 628 TACAA	Qy db
201 627	hrThrPheArgGlyArgIle CAGCCTTCAGAACAAGGATT	Cyst.	yGlnAlaArg ::: GCAAGCACAA	LSThrIleG1	AlaLeuSerGlyAlaHisThrIleGlyGlnAlaA ACTCTATCAGGAGCGCATACAATTGGGCAAGCAC	182 AlaLe	Фy
181 567	SerProArgAspMetThr ::: ::: ACAACAAAAGAACTCGTT	nGlyLeuSe :: AGGTTTCAC	eGlyArgGlnGlyLeuS 	uPh 	uGlyThrLeuIleSerLe 	162 SerLer ::: 508 AATCT	ОУ
161 507	ASnProProProProThrAla ::: GATTTGCCGGCTCCATTTTTT	A - H	rLeuAlaAsnSe CTCTGCTAACTO	aSe AAG	pSerThrThrAlaSerAl TCAACCACTGCAAGTTT	142 ArgAsp: 448 AGAGAC	Db dy
141 447	SerValProLeuGlyArg ::: AATGTGTTATTGGGAAGA	YProThrTrpSe ::: :: AGCAAGTTGGAA	yGl) AGG	pGlyThrAsnLeuLeuGl CTCTGTTGTTGCTCTAGG	laArgAspGlyTl TAGAGACTCTGT	122 AlaAla 388 GCTGC	Дy
12 38	snValGluAlaAlaCysProGlyValValSerCysAlaAspIleLeuAlaLeu ::	LSerCysAl TCTTGTGC	oGlyValVal GGTGTTGTT	LaAlaCysPros::	gAsnValGluAl : CCAAGTAGAGA(102 LysArc	gb Qy
101 327	luLysThrAlaGlyProAsnLeuAsnSerValArgGlyPheGluValIleAspThrIle 	yGlyPheGl \GGTTTTGA	nSerValArç :::: TCAATAAG <i>I</i>	COAsnLeuAsı AAATGCAAA	SThrAlaGlyPı SACAGCAGGTCO	82 GluLys 268 GAAAA	рb
81 26	\triangleright $ \bowtie$	1ASP \GATGATACATC	rIleLeuLeu : : : AGTGCTATT!	/SASPGlySel STGATGCATC	ysPheValGlnGlyCysAspGlySerIleLeuLeuAsp- CTTTGTTCAAGGATGTGATGCATCAGTGCTATTAGATG	66 CysPhe 208 TGCTT	g. Qy
65 20	LeuPhePheHisAsp CTTCATTTTCATGAT	LeuLeuAr CTTCTTCG	gMetGlyAlaSerLeuLeuArg	InAr	GlnalaValalaSerGluG] CTGCTGTCGCCAAAGAAG	46 GlnAla 148 TCTGCT	Qy
45 14	leValArgAlaAlaMetThr ::::::: ::: CAATTAAGTCAGCAGTGAAC	llnSerIleVa :: TTTCAACAAT	ProAsnLeuGlr CCAATGCACTT	rSerCysI : AAAATGTO	OThrPheTyrAlaSe :: TAATTTTTATGCCAC	26 ProTh	ДУ
25 87	aHisAlaGlnLeuSer GTCAGCTCAATTGTCA	Cysvalal ::: TTAGG	rLeuLeuSer	lAlavalse ; AGGA	tGlnCysLeuVa :: TATGTGTCTTAT	6 LeuMet ::: 46 ATATTT	ру
			-1116)	ARCPNC1 (1-	(1-313) × F	-047-825-4	US-10
	10 2		Indels: Gaps:	79%	57. 8	Match:	Query DB:

Search completed: May 3, 2003, 12:58:50 Job time: 2264 secs

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Command line parameters:

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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3, 2003, 11:27:38; Search time 190 Seconds (without alignments) 3709.871 Million cell updates/sec
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score

d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

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RESULT 1
AAH44077
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                                                                    Oryza sativa; modification;
                                                                                                    Oryza sativa peroxidase s4235 encoding cDNA SEQ ID NO:13.
                                                                                                                                                                          AAH44077 standard; cDNA; 1156
                                                                                                                              12-SEP-2001
                                                                                                                                                    AAH44077;
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                                                                                                                          (first entry)
                                                                     plant;
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            Location/Qualifiers 75..1058
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; bacterial infection; Magnaporthe grisca; ss.
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AAC51464
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AAX03970
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Oryza sativa perox
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Hiraga S;
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in rice under varying conditions
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                                                                   CysAspGlySerIleLeuLeuAsp-----
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CCGAACGCCAACTCGGTGCGCGGGTACGAGGTCATCGACGCCATCAAGGCGCAGCTCGAG
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pinus radiata; Monterey pine; ds.
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       Bloksberg LN,
                                                   09-OCT-1998;
14-JUL-1999;
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        Havukkala IJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase
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ThrTrpSerValProLeuGlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsn
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                                                                                        SerCysAlaAspIleLeuAlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyPro
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Hiraga S;
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            in rice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCACTCCGACCAGCAGCTCTTTAATGGAGGTTCTACAGATTCTCAGGTTACTGCGTAC
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of rice peroxidase under varying condicharacteristics -
                                             AAB99741.
                                                                                       Mitsuhara
                                                                                                                                                      2000WO-JP08728
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                                                                                                                                                                                                                                                                                                rice; peroxidase; POX; characteristic; gene expression; plant; bacterial infection; Magnaporthe grisea; ss.
                                                                                                                                                                                                                                            Location/Qualifiers 14..997
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AAH44071 to AAH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed
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                                                                                                                                                                     AlaCysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAspGlyThr 127
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ThrIleGlyGlnAlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThrAspIle
                                                                                                      AGCCTCAGCGGCGCAAACAACAACATCCCGCCGCCGACGTCGGGACTCGCCAACCTCACC
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                                                        SerLeuPheGlyArgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGlyAlaHis 187
                                                                                                                                      SerAlaSerLeuAlaAsnSerAsnProProProProThrAlaSerLeuGlyThrLeuIle 167
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The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL) coniferol glucosyl transferase (CCT), coniferin beta-glucosidase (CBG) laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,

methyl transferase,

CoA methyl

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                                                                                                             Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                    Claim 1; Page 189-190;
                                                                                                        structure
                                                                                                                                                                                           (GENE-)
                                                                                                                                                      WPI; 2000-317962/27
                                                                                                                                                                                                                        09-OCT-1998;
14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                          peroxidase nucleotide sequence SEQ ID NO:369
                                                                                                                                                                         Havukkala
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99US-0143811.
                                                                                                                                                                                                                                                                                                                              Monterey pine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coumerate CoA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The polynucleotides can be used for modulating lignin content, lignin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lignin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any organism and for PCR amplification. The lignin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and ABB16341 to AAB16449 represent polynucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1171
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                                                                                                                                     GTTGCACTTTCTGGCGGTCATACCATCGGGCAGGCGCAATGCAAGAATTTCAGAGCCCAT
                                                                                                                                                         ThrAlaLeuSerGlyAlaHisThrIleGlyGlnAlaArgCysThrThrPheArgGlyArg
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                                                                 ATTTACAACGAGACCAACATAGACAGTGCGTACGCCACTTCATTGCGTTCAAAGTGTCCG
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                                                                                                                                                                                                                                                                                                             Plant cell transformed with Stylosanthes humilis Shpx6 peroxidase useful to confer on plants resistance to fungi, e.g. Phytophthora parasitica, Leptosphaeria maculans or Sclerotinia scierctorium
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P-PSDB; AAW38217.
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This cDNA sequence includes a coding region for the 320-amino acid shpx6 peroxidase (see AAW38217) of Stylosanthes humilis. A claimed method of engineering a plant to fungal resistance comprises introducing into cells of the plant a DNA construct comprising a promoter that is constitutively operative in the plant cell (preferably the cauliflower mosaic virus 355 promoter) and the shpx6 sequence, or a hybridising sequence or fragment that encodes an enzyme with peroxidase activity. Also claimed are plant cells harboring the DNA construct, a plant comprising such cells, and material from such a plant, especially seed, pollen, a stem segment

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or a cutting. Resistance to fungi, especially Phytophthora parasitica, Leptosphaeria maculans or Sclerotinia sclerotorium, be conferred on cereal, legume, oilseed, sugar or fibre plants, particularly maize, banana, peanut, field pea, sunflower, tomato canola, tobacco, wheat, barley, oat, potato, soybean, cotton,
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PheAsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSerLeuPhe
                                                           ThrAlaTyrPheThrAsnLeuLeuSerArgGlyLeuPheHisSerAspGlnGluLeu
                                            AATGGTTACTATAAGAACTTGCTAGTGAAAAAGGGTCTCTTCCACTCTGATCAACAACTC
                                                                                                                 -----GlyGlyAspGlyAsnLeuAlaProIleAspValGlnThrProValArgPheAsp
                                                                                                                                                            ACTGAGAGCAACATAGATCCCAATTTTGCCAAATCATTGCAAGGAAATTGCCCTAATACC
                                                                                                                                                                                      GlyAspThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSer
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RESULT 6
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                                                                                       control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed. In the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the
                        pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the plants such as response to bacterial infection by Magnaporthe grisea.
                                                                                                                                                                                     The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AAH44071 to AAH44091. Also described are: (1) promoters for the
                                                                                                                                                                                                                                                           Claim 1;
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  bacterial infection; Magnaporthe
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Alignment Scores: Pred. No.:

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Length:

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                        ACCCAGGGGCAGATCAGGCTCAACTGCTCCAAGGTTAAC 1022
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US-10-047-825-4 (1-313) x AAH44082 (1-1171)
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Best Local Similarity:
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                                                                                                                                                        The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and crawfill fragments, where the sequences of the peroxidase genes in the set are given in AnH44071 to AAH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene capression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the peroxidase gene expression to impart particular characteristics to the
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                                                                                            No . :
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Mismatches:
Indels:
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Matches:
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LeuMetGlnCysLeuValAlaValSerLeu---LeuSerCysValAlaHisAlaGlnLeu

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RESULT 8
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  Plant; lignin;
Pinus radiata;
                                                                24-OCT-2000
                                      Eucalyptus grandis peroxidase nucleotide sequence SEQ
                                                                                           AAA68176
                                                                                                                    AAA68176 standard;
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                                                                                                                                                                                  ThrAlaGlyGlnIleArgArgAsnCysArgValValAsnSer
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                                                                (first entry)
lignin biosynthetic pathway; Eucalyptus Monterey pine; ds.
                                                                                                                   DNA;
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                                      ID NO:352.
             grandis;
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(CCR), phenyllanine ammonia lyase (PAL), 4 commarate (CCR), phenyllanine ammonia lyase (CAL), 4 commarate (CAR), phenyllanine ammonia lyase (CAR), 4 commarate (CAR), 2 coniferol glucosyl transferase (CGT), coniferon beta-glucosidase (CBG), CC confect acid methyl transferase, caffeoyl CoA methyl transferase, CCC commerate COA ligase, cytochrome P450 LXLA, diphenol oxidase, flavanol CCC commerate COA ligase, cytochrome P450 LXLA, diphenol oxidase, flavanol CCC commerate COA ligase, flavanoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The CCC polynucleotides can be used for modulating lignin content, ignin CCC composition and the structure of a plant, especially eucalyptus and pine CCC species, and for modifying the activity of an enzyme involved in lignin CCC content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any CCC cryanism and for PCR amplification. The lignin content can be efficiently CCC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAA68201 and AAB16341 to CCC exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4 hydroxylase (C4H), commarate 3 hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-COA reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 184; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure
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14-JUL-1999;
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99US-0143811.
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Sequence 1391 BP; 399 A; 321 ç; 307 G; 364 Ť 0 other;

Percent Similarity:
Best Local Similarity:
Query Match: Pred. No.: Alignment Scores: 4.09e-68 899.50 71.52% 56.96% 56.08% Conservative: Mismatches: Indels: Gaps: Length: Matches: 1393 180 46 85

US-10-047-825-4 (1-313) x AAA68176 (1-1391)

δã B Qγ 밁 Qy Вþ Ş 363 303 246 41 61 21 1 MetAlaSerProThrLeuMetGlnCysLeuValAlaValSerLeuLeuSerCysValAla ArgAlaAlaMetThrGlnAlaValAlaSerGluGlnArgMetGlyAlaSerLeuLeuArg HisAlaGlnLeuSerProThrPheTyrAlaSerSerCysProAsnLeuGlnSerIleVal ATGGTCGGCTTTTCCGTCGTCGTTGTCCTTGCCACTTCGGTTATCACC----ACTGCC LeuPhePheHisAspCysPheValGlnGlyCysAspGlySerIleLeuLeuAspAlaGly CGAGCTGGAGTAGCAAAAGCAATCAAGAATGAGACCCGGACGGGCGCGTCCTTJCTTCGG CGTTGTAAGCTCTCACCGAGTCATTATCAATCAACATGTCCGAAAGCATTGTCGATTGTT 80 422 40 60 362 302

s promoter, useful against nematode

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                                                                                                          Zea mays
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                                  24-NOV-2000;
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             24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the cDNA sequence of a peroxidase P7X gene. The P7X gene is isolated from maize inbred line Mp307. Peroxidases reduce hydrogen peroxide or molecular oxygen in the presence of an electron donor. Plant peroxidases are involved in pathogen defence responses. DNA constructs or transcription casset comprising peroxidase P7X gene and its promoter are useful for providing nematode resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1379
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AlaArgCysThrThrPheArgGlyArgIleTyrGlyAspThrAspIleAsnAlaSerPhe
                                              ArgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGlyAlaHisThrIleGlyGln
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The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set a given in AAH44071 to AAH44091. Also described are: (1) promoters for
                                                                                                                         New set of rice peroxidase genes in rice under varying conditions desired characteristics -
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P-PSDB; AAB99744.
                                                                                           Claim 1;
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                                    GlyGlyAspGlyAsnLeuAlaProIleAspValGlnThrProValArgPheAspThrAla
                                                                                                              GlyAspThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSer
                    GGCGGCGACACCAACCTGGCGCCGCTGGAC---TCCACCCCCAACGCCTTCGACAACGCC
                                                                                         GGCGAGTCCAACATCAACGCGCCGTTCGCGGCGTCGCTCCGGGCGAGCTGCCCGCAGGCC
                                                                                                                                                             CTCACTGGAGCGCACACGGTGGGCGTGGCGCAGTGCACCAACTTCCGGTCGCGGCTCTAC
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                                                                                  ArgAsnValGluAlaAlaCysProGlyValValSerCysAlaAspIleLeuAlaLeuAla
                                                                                                                                                CAGGGTGCGTTCCCTAATGTCAACTCGCTGAGGGGATTCGAGGTCATCTCTAGCATTAAG
                                                                                                                                                                                            LysThrAlaGlyProAsnLeuAsnSerValArgGlyPheGluValIleAspThrIleLys
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                                                                                                                         TyrPheThrAsnLeuLeuSerArgArgGlyLeuPheHisSerAspGlnGluLeuPheAsn
                                                                         AATGGTCCTACCGACTCGCTCGTCATAGCTTACAGCCACAATCTCAATGCCTTCTACCGC
                                                                                                                                                                                                                            TTCTACAAGCAACTTCTGAGCAAAAAAGGTTTGCTTACGTCAGACCAAGTCCTCTTTAAT
                                                                                                                                                              AspGlyAsn-----LeuAlaProIleAspValGlnThrProValArgPheAspThrAla
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27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999;

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66255 standard; DNA; 1220 AP. ANC36625; ANC36625; ANC36625; PROT-COTO (first entry) PROT-CO	PR 10-JJ PR 10-JJ PR 14-JJ PR 16-JJ PR 16-JJ PR 18-J PR 18-J PR 18-J				XX Arab DE Arab XX Hybr: KW Hybr: KW metal XX Arab XX EP10: XX EP10: XX 06-SI	C36
14488. **pathway; uence; ss.**	10-JUN-1999; 10-JUN-1999; 14-JUN-1999; 16-JUN-1999; 16-JUN-1999; 17-JUN-1999; 18-JUN-1999; 18-JUN-1999;	21 MAY -1999; 24 MAY -1999; 25 MAY -1999; 27 MAY -1999; 27 JUN -1999; 21 JUN -1999; 23 JUN -1999; 24 JUN -1999; 25 JUN -1999; 26 JUN -1999;	04 - MAY 1999; 05 - MAY 1999; 06 - MAY 1999; 06 - MAY 1999; 06 - MAY 1999; 07 - MAY 1999; 11 - MAY 1999; 11 - MAY 1999; 14 - MAY 1999; 14 - MAY 1999; 14 - MAY 1999; 14 - MAY 1999; 15 - MAY 1999; 16 - MAY 1999; 17 - MAY 1999; 18 - MAY 1999; 19 - MAY 1999;	25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; 01-APR-1999; 10-APR-1999; 11-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999;	Arabidopsis the Hybridisation protein ident. metabolic path Arabidopsis the EP1033405-A2. 06-SEP-2000.	
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                                                                                                                     standard;
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                                                    peroxidase nucleotide sequence SEQ ID NO:368
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    PheGluValI1eAspThrI1eLysArgAsnValGluAlaAlaCysProGlyValValSer

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53..148
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149..1051
                                                                                                                                        Location/Qualifiers 53..1054
                                                                                                                                                                                               gene; maize;
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                                                                                                                                                                                                corn; transgenic plant; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of a maize per5 cDNA clone encoding root preferential cattonic peroxidase (see AAW87893). The clone was isolated by screening maize root, stem, leaf, kernel and tassel RNA using probes (see AAV63718-19) based on tobacco peroxidase conserved domains. A probe generated from per5 cDNA was used to isolate the per5 gene (see AAV63717). Regulatory sequences of the per5 gene, including the promoter, introns and 3 untranslated region (3 UTR), argulated recombinant gene cassettes for controlling expression of recombinant gene sh selected tissue, especially the root, of transformed plants, particularly maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated regulatory sequences for transgenic plants - which are derived from the maize root preferential cationic peroxidase protein
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                                                                       ProThrTrpSerValProLeuGlyArgArgAspSerThrThrAlaSerAlaSerLeuAla
                                                                                                                  TTGGACAACAGCAGCATAGTTAGTGAGAAAGGGTCCAACCCGAACAGGAACTCCCTC
                                                                                                                                                                                                                                                                    LeuAspAlaGly---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrLeuMetGlnCysLeuValAlaValSerLeuLeuSerCysValAlaHisAlaGln---
                                                                                                                                                                              AGGGGGTTTGAGGTGATCGACCAGATTAAGGCTGCTCTTGAGGCTGCCCTGCCCAGGCACA 418
                                                                                                                                                                                                         ArgGlyPheGluValIleAspThrIleLysArgAsnValGluAlaAlaCysProGlyVal 112
                                                                                                                                                                                                                                                                                                                            SerLeuLeuArgLeuPhePheHisAspCysPheValGlnGlyCysAspGlySerIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTCCATGGGTTGTCTCGTCTTGCTCTGCCTTGTTTCTTCTCCCTTCCCAGTGCCGTC
AACAATGACATCCCAGCCCCCAACAACACCTCCCCCACTATCATCACCAAGTTCAAGCGC
                         AsnSerAsnProProProProThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArg
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Pareddy D,
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51.06%
51.25%
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RESULT 15
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ID ABN87
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XX 30-JU
XX ADN87
XX ACLI1U
XX LO11U
XX Cellu
KW Cellu
KW Celfe
KW Cinna
KW F5H;
KW Cinna
XX LO11U
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XX LO11U
XX LO11E
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XX ACRE
PR 29-SE
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PR 19-SE
PR 19-PST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1019
             Novel nucleic acid encoding lignification and cellulase enzymes their related enzymes useful for modifying lignin biosynthesis cellulose degradation in plants to manipulate plant cell wall
                                                                                                                                                                                                                                                                     04-APR-2002
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                                                                                                                         Spangenberg G,
                                                                                                                                                                                                                                      28-SEP-2001; 2001WO-AU01221
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DB; ABB78992.
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                                                                                                                                                                                                                                                                                                                                 perenne
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Claim 8; Fig 105; 436pp; English.

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a nucleic acid (I) or its fragment CC encoding caffeoyl-CoA 3-O-methyltransferase (CCOAMT), cinnamyl alcohol CC dehydrogenase (CAD), caffeia acid O-methyltransferase (OMT), commanded acid O-methyltransferase (OMT), commanded acid O-methyltransferase (OMT), peroxidase (CER), caffeia acid O-methyltransferase (OMT), peroxidase (CER), celulase (CAH), cinnamoyl-CoA reductase (CCR), peroxidase (CER), celulase (CAH), cinnamoyl-CoA reductase (CCR), peroxidase (CER), celulase (CAH), ferulate-5-hydroxylase (F5H), phenylalanine CC ammonia lyase (FAL) from perennial CC ryegrass (Lolium perenne) or fescue species. (I), its nucleotide columnonial sequence information and/or single nucleotide polymorphisms is useful as sequence information and/or single nucleotide polymorphisms is useful as molecular genetic marker. (I) can be used for modifying lignin CC biosynthesis and/or cellulose degradation in a plant to manipulate cell CC walls. (I) or its fragments are useful for isolating cDNAs and genes cencoding homologous proteins from the same or other plant short. Short CC segments of (I) or its fragment are useful in amplifyation protocols CC applify longer nucleic acids or its fragments encoding homologous CC genes from DNA or RNA. (I) or its fragments are useful as molecular CC genes from DNA or RNA. (I) or its fragments are useful as molecular CC usefunical stress for quantitative trait loci (QTL) tagging, QTL mapping, CC mechanical stress tolerance, disease resistance, insect pest resistance, CC plant stature, leaf and stem colour. The present sequence represents a CC Lolium perenne (perennial ryegrass) nucleotide sequence from the present CC invention.
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161 AlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAspMet 180 :::|||||| ||| ||||||
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                                                                                                                    ArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSerAsnProProProProThr 160
                                                                                                                                                                                                                        LeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThrTrpSerValProLeuGly ::::|||||||||
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-LOOPEXT=0 -UNITS-bits -START=1 = END=-1 -MATRIX-bitssum62 -TRANS-human40.cdi
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-USER-US10047825_@CGN_1 1_32_@runat_2604203_111959_7157 -NCPU=6 -ICPU=3
-NO_KLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR EILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11.
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                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
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ORGANISM: Pinus
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Sequence 369, Application US/0961519
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GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
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US-09-615-192A-369
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LENGTH: 1171
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CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
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PRIOR FILING DATE: 1997-
PRIOR APPLICATION UNMBER:
DRIOR ETITION DATE: 1000
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CTAGCTTCGTGGGCAGAAAACAGCAGCTCCGAACAACAATTCCGTGAGAGGGGTTCGAA
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                                                                    CTGCACTTCCATGACTGCTTCGTCAATGGGTGCGATGCGTCGATATTGTTGGATGACACG
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                  -GlyGluLysThrAlaGlyProAsnLeuAsnSerValArgGlyPheGlu 96
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US-09-615-192A-368
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                                                                                                               SOFTWARE: F
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                                                                                                                                                                           PRIOR EILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR EILING DATE: 1996-00-17
PRIOR APPLICATION
                                                                                                                                                                                                                              APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Maderials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin C
FILE REFERENCE: 11000.1003c4U
CUGRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
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         Sequence 5, Application US/09097319A
Patent No. 6384207
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
 APPLICANT:
                                                                                                                                    784 CACTCCGACCAGCAGCTG
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APPLICANT:
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STATE: Indiana
COUNTRY: USA
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LENGTH: 1354 base pair
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/097,319A
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ValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGly 132
                                                                               TTGGACAACAGCAGCATAGTTAGTGAGAAAGGGTCCAACCCGAACAGGAACTCCCTC
                                                                                                                                   TCTTTAGTCAGACTGCATTTCCATGACTGCTTTGTCAAGGGCTGCGATGCTTCGGTGCTG
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9330 Zionsville Road
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Petolino, Joseph F.
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR TILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
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; Sequence 361, Application US/09615192A
; Patent No. 6410718
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                                                                                              ; TYPE: DNA; ORGANISM: Pinus radiata US-09-615-192A-361
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    Percent Similarity:
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                                                                                                                                                           SEQ ID NO 361
LENGTH: 916
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin (FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
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Query Match:
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Sequence 3, Application US/
Patent No. 6278041
GENERAL INFORMATION:
APPLICANT: Lagrimini, Mark
APPLICANT: Desai, Nalini
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US-10-047-825-4 (1-313) x US-09-365-150-3 (1-975)
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Best Local Similarity:
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: sylvestris peroxidase gene
US-09-365-150-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6278041el Peroxidase FILE REFERENCE: S-31081pl CURRENT APPLICATION NUMBER: US/09/365,150 CURRENT FILING DATE: 1999-07-30 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 975
TYPE: DNA
ORGANISM: Artificial Sequence
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ACCAACCTGGACATCAGCACCCCCAACGACTTCGACGACTACTTCACCAACCTCCAG
                                                                                                                                                                                                                                  CTGACCGACCTGGTGGCCCTGAGCGGCGCCCACACCTTCGGTCGAGCCCGCTGCGGCACC
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                                   AlaProIleAspValGlnThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeu
                                                                           ACCTTCCTGCAGACCCTCCAGGGCATCTGCCCCCAGGGCGCAACAACGGCAACACCTTC
                                                                                                              SerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGlyAspGlyAsn---Leu
                                                                                                                                                        TTCGAGCAGAGACTGTTCAACTTCAACGGCAGCGGCAACCCCGACCTGACCGTGGACGCC
                                                                                                                                                                                          PheArgGlyArgIleTyrGly-------AspThrAspIleAsnAla
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                                                                                                                                                                                                                                                                                                             CCCAGCCCCTTCGAGACCCTGGCCGTGATGATCCCCCAGTTCACCAACAAGGGCATGGAC
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                                                          US-10-047-825-4 (1-313) x US-08-378-588-23 (1-1270)
                                                                                                   Query Match:
                                                                                                                 Best Local Similarity:
                                                                                                                                                 Score
                                                                                                                                                                            Alignment Scores:
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US-08-378-588-23
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                                                                                                                                                               Pred. No.:
                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                         TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TOPOLOGY:
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STREET: Pinckney
STREET: P.O. Box
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STRANDEDNESS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 53701-2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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DEDNESS: double
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721.50
63.92%
47.78%
44.98%
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                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                   Sequence 23, Application US/08811094
Patent NO. 5869720
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PE
                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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             :: Nicholas J. Seay, Quarles & Brady First Wisconsin Plaza, One South
Pinckney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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APPLICATION NUMBER: 08/378,588
FILING DATE: 25-JAN-11995
ATTORNEY/AGENT INFORMATION:
NAME: Seary Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pair
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CITY: Ma
STATE: W
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         162 ACTGATGCTCGAGCTGGTGCTAAAATTATTCGTCTTCATTTCCATGATTGTTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LeuValAlaValSerLeuLeuSerCysValAlaHisAlaGlnLeuSerProThrPheTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                              ProAsnLeuAsnSerValArgGlyPheGluValIleAspThrIleLysArgAsnValGlu 106
                                                                                                                                                                                                                                                                                                     GlyCysAspGlySerIleLeuLeuAspAlaGlyGly------GluLysThrAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaSerSerCysProAsnLeuGlnSerIleValArgAlaAlaMetThrGlnAlaValAla :::::::|||||||||||::: ||||||||||||
AlaSerAlaSerLeuAlaAsnSerAsnProProProProThrAlaSerLeuGlyThrLeu 166
                                                                                                                                                                                                                                                                                                                                                                              SerGluGlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGln
                                                         GTTGTCTTGGCTAAAGGTCCGTCGTGGCAAGTACTTTTTGGCAGAAGAGATAGCTTAACA
                                                                             ThrAsnLeuGlyGlyProThrTrpSerValProLeuGlyArgArgAspSerThrThr
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DNA (genomic)

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PCT-US94 11121-23

; Sequence 23, Application PC/TUS9411121

; GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.

TITLE OF INVENTION: TRANSGENIC COTTON PLANTS

TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE

NUMBER OF SEQUENCES: 23
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                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-2:
TELECOMMUNICATION INFORMATION:
TELEFONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION: FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                               STREET: PINCKNEY St.,
STREET: PINCKNEY St.,
STREET: PO. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
DOTTICATION THE PROPERS OF THE PROPERS 
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            879 CAAAGTCAGTTTTTTGATGATTTTATTTGCTCGATGATTAAATTGGGTAATATAAGTCCA
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                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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irst Wisconsin Plaza, One South
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Percent Similarity:
Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/365,150
CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 975
TYPE: DNA
ORGANISM: Nicotiana tomentosiformis
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APPLICANT: Desai, Nalini
TITLE OF INVENITON: No. 6278041el Peroxidase
FILE REFERENCE: S-31081P1
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                                                                                                                                                                                    ThrAsnLeuLeuGlyGlyProThrTrpSerValProLeuGlyArgArgAspSerThrThr 146
                                                                                                                                                                                                                  AATGTATGCCCTGGTGTTGTATCTTGTGCAGATATTTTATCCCTTGCATCTGAAATTGGA
                                                                                                                                                                                                                                    AlaAlaCysProGlyValValSerCysAlaAspIleLeuAlaLeuAlaAlaArgAspGly 126
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                                                                                                                                                                                                                                                                                                                                             GGTTGTGATGGATCCATTTTATTAGACACAGATGGGACTCAAACTGAGAAAGATGCAGCT
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HisThrIleGlyGlnAlaArgCysThrThrPheArgGlyArgIleTyrGly-----
                                                                                          GCAAACCGATCTGAAGCTAATAGTGATATCCCCCAGCCCCTTTGAAACCCCCTGCTGAATG
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                               ACACCACTATTCACCAACAAGGGAATTGGATCTTAACTGATCTTGTTGCTCAATCAGGTGCA
                                                          IleSerLeuPheGlyArgGlnGlyLeuSerProArgAspMetThrAlaLeuSerGlyAla 186
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CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 975
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APPLICANT: Lagrinini, Mark
APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6278041el Peroxidase
FILE REFERENCE: S-31081P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLeuPhe-----AsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSer 276
                                                   ACCGACGCCCGCCGGCGCCCAAGATCATCCGCCTGCACTTCCACGACTGCTTCGTGAAC
                                                                                                                                                AlaSerSerCysProAsnLeuGlnSerIleValArgAlaAlaMetThrGlnAlaValAla 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAACTGGTACTAATGGAGAAATTAGGACAGATTGCAAGAGGGTTAAT
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                                                                                  SerGluGlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGln 69
                                                                                                                    GACAGCACCTGCCCCAACGTGACCAGCATCGTGCGCGGCGTGATGGACCAGCGCCAGCGC
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Matches:
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TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Control of File Reference: 11000.1003c4U CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR FILING DATE: 1907-11-21 PRIOR ETLING DATE: 1997-11-21 PRIOR ETLING DATE: 1997-11-3,000 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR ETLING DATE: 1998-09-11 PRIOR APPLICATION NUMBER: US 09/169,789 PRIOR FILING DATE: 1998-10-09 NUMBER OF SEO ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 371
LENGTH: 1522
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-615-192A-371
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Sequence 371, Application US/09615192A Patent No. '6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGACCGGCACCAACGGCGAGATCCGCACCGACTGCAAGCGCGTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAACGTGGGCGCC---GGCGGCTTCGACATCGTGGACGACGACATCAAGACCGCCCTCGAG 324
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Havukkala, Ilkka
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US-09-615-192A-371
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      CTCTTCTTTGAACAGTTTGTGCTGAGCATGCTCAAAATGGGGCAGCTGGATGTGCTCACA
                             LeuPheAsnAlaAspPheValAlaAlaMetIleArgMetGlyAsnValGlyValLeuThr
                                                                                 ACTCTTTACACCGACACTCGAACCCGCGACATTGTGATCAATTTTGCGGTGAAICAGAGC
                                                                                                          GluLeuPheAsnGlyGlySerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSer
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US-09-097-319A-1
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TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO:
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                                                                                             FEATURE:
NAME/KEY:
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STATE: Indiana
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NAME: Stuart, Donald R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/097,319A
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MOLECULE TYPE:
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LOCATION: 4201..4425
OTHER INFORMATION: //
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                              LOCATION:
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9330 Zionsville Road
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VENTION: Regulatory Sequences for Transgenic Plants
EQUENCES: 59
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Hopkins, Nicole
Menke, Michael A.
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TTACATGTGTAGGGCTGCGATGCTTCGGTGCTGTTGGACAACAGCAGCAGCATACTTAGT 5106
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                                                                                                                        ATTGGAGCTCTCAGTGCAACGCATGTGCTCTGTAATCTACTGTCACCACTACTCTGTAGT 4986
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                                                            GTGTGCTTAAACTCTAAACTATTCCACGTGGCTAGTAATTACCAATCATTTACAACACTG 5046
                                                                                                                                                                                  ATAAGATGTCCTTTTTTTGAGCCACTCGAGAAGATGTTTACTTAACTCTAGTGCGCAATG 4926
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Content

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US-09-615-192A-365
Sequence 365, Application US/09615192A
Patent NO. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard APPLICANT: Havukkala, Ilkka TITLE OF INVENTION: Materials
                                                                                                                                                                    6006 CCACTGACAGGGTCACAAGGTGAGATCAGGAAGAACTGCAGGAGGCTCAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValLeuThrGlyThrAlaGlyGlnIleArgArgAsnCysArgValValAsnSer 313
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   Materials and Methods for the
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Best Local Similari
Query Match:
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CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Pinus
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                                                                                                                                    LeuSerProArgAspMetThrAlaLeuSérGlyAlaHisThrIleGlyGlnAlaArgCys 194
                                                                                                                                                                                     TGGACAGTGCTTGGAAGGAGAGACTCAGCAACTGCCAGCCTAAGCGCCGCAAACACC
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    2003, 12:58:59; Search time 108 Seconds
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4884	Result No.
808 801 765.5 753.5	Scor
50.4 49.9 47.7 47.0	Query Query Match Length DB ID
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US-09-938-842A-1711 US-09-938-842A-60 US-09-938-842A-1714 US-09-938-842A-1780	DB ID
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	361,	75,	83, 7	989,	353,	217,	1458,	858,	50,	equence 2184,	2209,	equence 218	166,	equence 1548,	sequence 2079, Ap	equence 1549,	682,	2329,	1078,	e 2446,	257	-	2693,	119	1498,	equence 2367,	1340,	Sequence 1596, Ap	11,	equence 783,	equence 1518	equence 2559,	1457; A	1719, 1	3, App	Appli	e 3, Appl	1632, A	Sequence 2325, Ap	e 1273, A	equence 2545, A

ALIGNMENTS

US-09-938-842A-1711

GENERAL INFORMATION:

Sequence 1711, Application US/09938842A Patent No. US20020160378A1

; ORGANISM: Arabidopsis thaliana US-09-938-842A-1711 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 1711 LENGTH: 996 APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
APPLICANT: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
CURRENT FILING DATE: 2001-08-24 CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22 TYPE: DNA

Alignment Scores

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              LeuThrGlyThrAlaGlyGlnIleArgArgAsnCysArgValValAsnSer
                                               CAAGGAGAGTTTTTTGAGCAATTTGCGGAATCGATCAAGATGGGAAATATCTCTCCCC
                                                                       AlaSerLeuPheAsnAlaAspPheValAlaAlaMetIleArgMetGlyAsnValGlyVal
                                                                                                CAAGTTCTGTTCAGCAGTAACGAGAAATCGAGAGAGCTTGTGAAGAAGTATGCAGAAGAT
                                                                                                                        GlnGluLeuPheAsnGlyGlySerGlnAsp---AlaLeuValArgGlnTyrSerAlaSer
                                                                                                                                                 AGCTTCGACAACAGCTACTTCAAGAACTTGATAGAGAACAAGGGGGTTGTTGAACTCGGAC
                                                                                                                                                                ArgPheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGlyLeuPheHisSerAsp
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER: OS 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: OS SEQ ID NOS: 5379
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-60
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US-09-938-842A-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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LENGTH: 1017
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                                                                                                                                             GlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSerAsnProProProPro 159
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                 GAGATCAAGGCAGCATTAGAGAACGAATGCCCTAACACTGTTTCTTGTGCTGATGCCTTA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAGCCAAAGCTGTTGCAAGGGAGACTCGTATGGCTGCTTCTCTCATGAGGCTCCATTTC
                                                              ACCACCTTTCAACACAATTGTCACGAGATTTAACAACCAAGGTCTCGATCTCACCGAC
                                                                                                                                                                                              ACTCTAGCCGCTAGAGACTCCTCTGTTCTTACTGGTGGACCAAGCTGGATGGTTCCTTTG
                                                                                                                                                                                                               AlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThrTrpSerValProLeu 139
                                                                                                                                                                                                                                                                             ThrIleLysArgAsnValGluAlaAlaCysProGlyValValSerCysAlaAspIleLeu 119
                                                                                                                                                                                                                                                                                                                            GTTACTGAGAAGAACTCTAACCCGAACAGCAGATCGGCTCGCGGGTTTGAAGTTGTTGAC
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                                                                                               ThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAsp
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Pred. No.:
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1714
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                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1714, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: STRESS-REGULATED GENES TITLE OF INVENTION: SAME, AND METHODS OF U FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
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CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 .
                                                                                  TITLE OF INVENTION: STRESS-REGULATED GENES OF TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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Best Local Similarity:
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SEQ ID NO 1980
LENGTH: 1077
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-06-22
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APPLICANT: HATCH JOIN
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Thu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIF1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-06-24
PRIOR FILING DATE: 201-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2545
LENGTH: 1011
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Query Match:
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Alignment Scores: Pred. No.: Score:
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                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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APPLICANT: Kreps, Joel
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ArgValValAsnSer
                                                                         IleArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIleArgArgAsnCys 308
                                                                                                                 CTAGTGGAGGCTTATAGTCGGAGCCAGAGCTTGTTTTTCAGGGACTTCACATGTGCGATG
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                                                    ATCAGAATGGGAAACATTTCG-
                                                                                                                                                 LeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPheValAlaAlaMet
                                                                                                                                                                                  CTTTTGAGTTCTGATCAGATTCTGTTCTCGAGTGACTTAGCCGTGAACACCACAAAGAAA
                                                                                                                                                                                                                  LeuPheHisSerAspGlnGluLeuPheAsnGly------GlySerGlnAspAla
                                                                                                                                                                                                                                                     AGGAGCACTACGGACACCTTCGACAACAATTATTTCAAGAACCTGCTTGAAGGAAAAGGT
                                                                                                                                                                                                                                                                                  ValGlnThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGly
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2325
LENGTH: 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: STRESS-REGULATED GENES OF TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kreps, Joel APPLICANT: Wang, Xun APPLICANT: Zhu, Tong
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                                                                                                               394 ATCGCAGCTCAACAAGCTGTAAATTTGGCAGGAGGTCCTTCTTGGAGGGTTCCTTTGGGG
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AlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSer---ProArgAsp 179 :::||| ||| ||| |||
                                                  AGAAGAGATAGCTTACAAGCATTCTTTGCTCTCGCTAATACAAATCTTCCCGCTCCATTC
                                                                                                                                  LeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThrTrpSerValProLeuGly 140
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CURRENT EILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                              SEQ ID NO 1632
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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US-10-101-736-3
                        Sequence 3, Application US/10101736
Publication No. US20030041351A1
GENERAL INFORMATION:
APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo APPLICANT: Co., Ltd.); Randy Dale Allen (Texas tech University)
TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics
TITLE OF INVENTION: for producing cotton fibers from these cotton plants
CURRENT APPLICATION NUMBER: US/10/101,736
                FILE REFERENCE:
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; PUBLICATION IMPORMATION:
; AUTHORS: Kazuhito FUJIYAMA et al.
; TITLE: Structure of the horseradish peroxidase
; JOURNAL: European Journal of Biochemistry
; VOLUME: 173
; PAGES: 681-687
; DATE: 1988
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TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics
TITLE OF INVENTION: for producing cotton fibers from these cotton plants
FILE REFERENCE: 204552015600
CURRENT APPLICATION NUMBER: US/09/834,659
CURRENT FILLNG DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US/09/347,669
PRIOR APPLICATION NUMBER: US/09/347,669
RIGH APPLICATION NUMBER: US/09/347,669
RIGH APPLICATION NUMBER: US/09/347,669
RIGH FILING DATE: 1999-07-05
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 3
LENGTH: 1062
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LOCATION: (1)...(1062)
PUBLICATION INFORMATION:
AUTHORS: Kazuhito FUJIYAMA et al.
TITLE: Structure of the horseradish peroxidase isozyme
JOURNAL: European Journal of Biochemistry
VOLUME: 173
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                                                                                        GENERAL INFORMATION:

APPLICANT: Yoshihisa KASUKABE, Izumi IHARA, Yoshihiko MAEKAWA (Toyobo Co., Li
APPLICANT: Randy Dale Allen (Texas tech University)

TITLE OF INVENTION: Cotton plants with improved cotton fiber characteristics

TITLE OF INVENTION: producing cotton fibers from these cotton plants
CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-0 NUMBER OF SEQ ID NOS: 3 SEQ ID NO 3
                                                                                                                                                                                         Sequence 3, Application US/09834656 Patent No. US20020049999A1
                                                                           FILE REFERENCE:
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LOCATION: (1)...(1062)
PUBLICATION INFORMATION:
AUTHORS: Kazuhito FUJIYAMA et al.
TITLE: Structure of the horseradish peroxidase isozyme
JOURNAL: European Journal of Biochemistry
VOLUME: 173
PAGES: 681-687
DATE: 1988
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                                  ThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGly
                                                                     AATCAGTGTCGGTTTATTATGGACAGATTATACAACTTCAGCAACACCGGTTTACCCGAT
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                                                                                                                                                                      GlnGlyLeuSer---ProArgAspMetThrAlaLeuSerGlyAlaHisThrIleGlyGln 191
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Query Match:
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LENGTH: 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: STRESS-REGULATED GENES TITLE OF INVENTION: SAME, AND METHODS OF UPILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Xun APPLICANT: Zhu, Tong
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PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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RESULT 13
US-09-938-842A-1457
: Sequence 1457, Application US/09938842A
: Patent No. US20020160378A1
                                        PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1457
LENGTH: 1062
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                   APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Du, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
       ORGANISM: Arabidopsis thaliana
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ArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIleArgArgAsnCysArg 309
                                                                  ValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPheValAlaAlaMetIle
                                                                                                   ValGlnThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeuSerArgArgGly
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                                                                                                                                                                        CTACGTACGCCTACGGTTTTCGACAACAAATACTACGTGAATCTCAAAGAGCGAAAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSerAsnProProProProThr
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                                                                                                                                   LeuPheHisSerAspGlnGluLeuPhe-----AsnGlyGlySerGlnAspAlaLeu
                                                                                                                                                                                                                                                                        AlaLeuArgGlnGlnThrCysProArgSerGlyGlyAspGlyAsnLeuAlaProIleAsp
                                                                                                                                                                                                                                                                                                           AGATTATACAATTTCAGCAACACAGGTTTACCCGACCCTACACTCAACACTACTTACCTC
                                                                                                                                                                                                                                                                                                                                            ArgIleTyrGly---
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Matches:
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US-09-938-842A-2559
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DB:
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Best Local Similarity:
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LENGTH: 1011
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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APPLICANT: Kreps, Joel
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160 ThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerProArgAsp 179
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                                                                                                                        ACAATTGGTGCTAGAGATGCTACAATCCTGGTGGGTGGGCCTTACTGGGATGTTCCTGTG 447
                                                                                                                                                           AlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThrTrpSerValProLeu 139
                                                                                                                                                                                                                         ThrileLysArgAsnValGluAlaAlaCysProGlyValValSerCysAlaAspIleLeu 119
                                                                                                                                                                                                                                                                                 CACGACTGCTTTGTCCAAGGATGTGATGGATCGGTGTTGCTAGACGAGACAGAAACTCTA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSerAsnProProProPro 159
                                                                                                                                                                                                    AGAATCAAGAACATAATCGAATCCGAATGTCCTGGAGTTGTTTCATGCGCTGATCTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAATGCATAGTGAAGGAAGATCCTAGAAATGCAGCCATAATTATTCGTCTTCACTTC
                                             GGAAGAAAAGATTCAAAAAACCGCAAGCTACGAGCTTGCCACAACAAACCTTCCAACTCCA
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                                                                                                                                                                                                                                           ; SEQ ID NO 1518;
LENGTH: 987;
TYPE: DNA;
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1518
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                                             US-10-047-825-4 (1-313) x US-09-938-842A-1518 (1-987)
                                                                                                     Query Match:
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Best Local Similarity:
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Patent No. US20020160378A1
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                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: STRESS-REGULATED GENES OF TITLE OF INVENTION: SAME, AND METHODS OF USE
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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        CysLeuValAlaValSerLeuLeuSerCysVal--
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973 TCTGCGGTTAAT 984
                                                                                              289 IleArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIleArgArgAsnCys 308 :::|||||| ||| |||
                                                                                                                                              793 CGTGGGCGTGGAGTTCTCCAATCCGATCAAGTCCTTTGGACCGATCCAGCCACTAGACCC 852
                                                                                                                                                                                                                                                   673 CCAACATTTTTGGCGCAGCTTCAAACACAATGTCCCCAAAACGGCGACGGTTCAGTGCGC 732
                                                                                                                                                                                                                                                                                                                                                      269 LeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPheValAlaAlaMet 288
                                                                                                                                                                                                  733 GTGGATCTCGACACCGGAAGCGGAAGCACTTGGGACACTTCTTACTACAACAACCTAAGC 792
                                                                                                                                                                                                              229 AlaProIleAspValGlnThrProValArgPheAspThrAlaTyrPheThrAsnLeuLeu 248
                                                                                                                                                                                                                                                                          209 AlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGlyAspGlyAsnLeu 228
                                                                                                                                                                                                                                                                                                                         493 AATCTCCCTGGTCCCCGTGACTCCGTTGCCGTTCAACAACAGAAATTCTCCGCCTTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 AsnProProProProThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGly 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 TrpSerValProLeuGlyArgArgAspSerThrThrAlaSerAlaSerLeuAlaAsnSer 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 CysAlaAspIleLeuAlaLeuAlaAlaArgAspGlyThrAsnLeuLeuGlyGlyProThr 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 PheGluValIIeAspThrIIeLysArgAsnValGluAlaAlaCysProGlyValValSer 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 LeuGlnSerIleValArgAlaAlaMetThrGlnAlaValAlaSerGluGlnArgMetGly 55
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                        ArgValValAsn 312
                                                                                                                                                                       SerArgArgGlyLeuPheHisSerAspGlnGluLeuPheAsnGlyGlySerGlnAspAla 268
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                                             TTTGAAGTCATAGACAACGCCAAAACGCAGCTCGAAGCCGCGTGTCCTGGAGTTGTCTCT 375
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Search completed: May 3, 2003, 13:53:55
Job time: 114 secs

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Command line parameters:

WODEL=frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPT0_spool/US10047825/runat_26042003_112042_7654/app_query.fasta_1.455
-DB-EST -QFMT-fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START-1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=quality -THR_MIN=16 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=axt -HEAPSIZE=500 -MINLEN=0 -MAXEN=200000000
-USER=US10047825_eCGN_1_1_1456_erunat_26042003_112042_7654 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPO=60 -XGAPEXT=60 -FGAPEXT=7
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Fgapop 6.0 , I
Delop 6.0 , I
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE	SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 BG842311 LOCUS DEFINITION		44	4 4 3 2	40 41	398	37	ა ა რ თ	34	ယ ယ ယ လ	. ω : - μ :	30 30	28	26	25	23	21 22	20	18	15 17	15	. 13	12	10	,	8 7	თ u	О л 4		νÞ	Result No. (
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iopsida; Zea.	ophyta;		mRNA cDNA clone	NTS																													
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	Tracheophyta;		9-MAY-2001 mRNA		PI1_96_A0 · PI1_71_G0	PI1_79_G1 LG1 357 F	PI1_69_G0	PI1_69_D1	PI1_80_B0	DG1_57_G0	LG1_357_F	EM1_45_F1 EM1_47_E1	LG1_349_F	DG1_85_C0	DG1_86_C0	DG1_30_A0	DG1_21_H1	PI1_31_A0	DG1_82_H0 PI1_79_G1	P11_79_D1	PI1_56_H0	DG1_18_A1	PI1_32_E1	PI1_88_F0	PI1_80_B0	PI1_96_A0 PI1_42_B1	PIC1_31_D	EM1_60_C0	PI1_31_A0	ST	EST27	EST29-	

AUTHORS

Qiu, F., Cui, F., Guo, L., Ashlock, D.A, Wen, T.J. and Schnable, P.S.

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                                                                                                                                                                                                                                                                                                                                            205 ThrAspIleAsnAlaSerPheAlaAlaLeuArgGlnGlnThrCysProArgSerGlyGly 224
                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                             3 ACCGACATCAACGCCTCCTTCGCGGCGCCTGCGGCAGCAGACGTGCCCGCGGTCCGGCGGC
                                                                                  ValAlaAlaMetIleArgMetGlyAsnValGlyValLeuThrGlyThrAlaGlyGlnIle 304
                                                                                                                                                 SerGlnAspAlaLeuValArgGlnTyrSerAlaSerAlaSerLeuPheAsnAlaAspPhe
                                                                                                                                                                                                                                                                              AspGlyAsnLeuAlaProIleAspValGlnThrProValArgPheAspThrAlaTyrPhe
                  ArgArgAsnCysArgValValAsnSer 313
                                                                                                                                                                                              ACCAACCTGCTGTCGCGGAGGGGCCTGTTCCACTCGGACCAGGAGCTCTTCAACGGCGGG
                                                                                                                                                                                                                                                               GACGGCAACCTGGCCCCATCGACGTGCAGACGCCGGTGAGGTTCGACACGGCCTACTTC
                                                                 GTGGCAGCCATGATTAGGATGGGCAACGTTGGGGTGCTCACCGGCACCGCTGGACAGATC 302
                                                                                                                                TCGCAGGACGCCTGGTGAGGCAGTACAGCGCCAGCGCCTCGCTCTTCAACGCCGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14208633
Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G405 Agronomy, Iowa State University, Ames, IA 50011-1010, Tel: 515-294-0975
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 515-294-2299
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Research 6: 791-806, 1996)."
162 c 153 g 102 t
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/tissue_type="Seedling and silk"
/lab_host="DH10B"
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AA979912.1
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BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
BACKWARD: T0 column: 6
Plate: MEST3 row: D column: 6
Seq primer: tw1412 (5'-GAAGATACCCCAACCAACC-3').
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l: schnable@lastate.edu
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                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: green seedlings; vector: pAD-GAL4; Site_1: ECORI, Site_2: XhoI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA polI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZAP lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
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/clone="MEST3-D6"
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/cultivar="B73"
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ThrAsnLeuLeuGlyGlyProThrTrpSerValProLeuGlyArgArgAspSerThrThr 146

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BG841858.2
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MEST27-D09.T3
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Agronomy, Iowa State University,
515-294-0975
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                                                                                                                                                                                                                                            schnable@iastate.edu
                   /tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                               /clone_lib="ISUM4-TN"
                                                                                                                         /clone="MEST27-D09"
                                                                                                                                    /db_xref="taxon:4577"
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Iowa State University
G405 Agronomy, Ames, 1
Tel: (515)-294-0975
                                                Expressed Sequence Tags
Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory
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Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Maize Seedlings
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                                                                                                                                                                                                                                                                               T18410 230 bp mRNA linear EST 17-OCT-1996 6c02d10t7 etiolated seedling Zea mays cDNA clone 6c02d10 5' end similar to similar to peroxidase, mRNA sequence.
 Plant
                                                                    Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T., Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                        Zea mays
                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                Zea
                                                                                                                                                                                                                                T18410.1 GI:474233
EST.
                                   Partial sequencing and mapping of clones
                                                                                                                               clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                       T18410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
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                                                                                                                (bases 1 to 230)
                                                                                                                                                                                                              mays.
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 Mol. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an Xhol oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with Xhol and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZap lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECCRI; Site_2: XhoI; ds-cDNA molecules were generated as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
/clone="MEST3-D6"
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/cultivar="B73"
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1085-1101 (1994)
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RESULT 6
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                                                                                                                                             21 HisAlaGlnLeuSerProThrPheTyrAlaSerSerCysProAsnLeuGln 37
                                                                                                                                                                                     58 ATGGCGTCTCCCACCTTGATGCAATGCCTGGTCGCCGTTTCCCTCCTCTCTGTGTCGCC
                                                                                                                                                                                                          CACGCACAGCTCTCGCCCACGTTCTATGCGTCCTCCTGCCCCAACCTGCAG 168
BE366146 369 bp m
PI1_31_A02.b1_A002 Pathogen induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gainesville, FL 32611-(
ph: 904-392-1928, ext.
fax: 904-392-4072
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University of Arizona, Tucson,
Dept. of Plant Sciences, University of Arizona, Tucson,
ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interdisciplinary Center for Biotechnology Research
DNA Sequencing Core
University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biological Sciences, School of Science California State University, Hayward Hayward, CA 94542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-mail: robferl@nervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayward, CA 9454
ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helentjaris TG (primary contact)
Dept. of Plant Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: ZipLox; Site_1: Sall; Site_2: NotI; oligo-dT selected mRNA was prepared from above-ground tissue from10 day-old eticlated seedlings. ds-cDNA was prepared by priming with a NotI oligo-dT oligomer and the second strand by RNase-nicking of the DNA:RNA hybrid with DNA POlI fill-in. Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             individually analyzed.
82 c 60 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          size-selected.
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/clone="6c02d10"
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/lab_host="DH10B"
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1928, ext. 301
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                                                                                                                                                                                                                                                                                                                                                                                          Length:
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mRNA linear EST 20-JUL-2000
1 (PI1) Sorghum bicolor cDNA,
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                     linear
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RESULT 7
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                                                                                     AspGlySerIleLeuLeuAspAlaGlyGlyGluLysThrAlaGlyProAsn 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
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BE366146.1
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Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clade; Panicoideae; Andropogoneae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An EST database from Sorghum: pathogen-induced plants
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706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 two-week-old sorghum plants 48 hr after inoculation; vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; Two-week-old sorghum plants (BTX 623 cultivar) were infected with pathogen (isolate FRM42I of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be secuenced were accompanion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequenced were prepared by mass excision. WARNING: Whost or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/note="Organ: Anthracnose-infected leaves from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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125 c
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    mRNA
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TITLE
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BG411665
BG411665.1
                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 434)
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                 sorghum.
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                               AW287460 434 bp
LG1_228_C02.b1_A002 Light Grown
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d,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Embryo1 (EML)"
/clone_Togan: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryology germinate
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                                                           Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                           Unpublished (2002)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 476)
Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C.,
Sudman, M. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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Sorghum bicolor
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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On Jan 6, 2000 this sequence version replaced gi:6677304.
Contact: Cordonnier-Pratt MM
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Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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706 542 1860
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//clone_lib="Light Grown 1 (LG1)"
//note="Organ: 10- to 14-day-old light-grown (greenhouse)
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/db_xref="taxon:4558"
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B Qy 밁 Qy

COMMENT

TITLE JOURNAL

An EST database from Sorghum: pathogen-induced Unpublished (2000) Contact: Cordonnier-Pratt MM

plants

Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 CAGAGGATGGGCGCCTCTCTGCTCAGGCTCTTCTTCCACGACTGCTTTGTTCAAGGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 GlnArgMetGlyAlaSerLeuLeuArgLeuPhePheHisAspCysPheValGlnGlyCys
                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or 77 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV
  1 (bases 1 to 479)
Cordonnier-Pratt, M.-M.,
                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                     BE601026 479 bp II_96_A03.b1_A002 Pathogen induced
                                                                                                              Sorghum bicolor
                                                                                                                                        sorghum.
                                                                                                                                                                                     BE601026.1
                                                                                                                                                                                                             BE601026
                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // notes Wector: pBluescript II SK(-) from Lambda Zap II;
// site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old sm4A2I, a sorghum isolate of the anthracnose
pathogen Colletotrichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-a RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host olant no effort was made to all interests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the host plant, no effort was made to eliminate ESTs deriving from the pathogen." a 164\ c 138\ g 96\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colletotrichum graminicola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sorghum bicolor"
/cultivar="BTx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Pathogen-infected compatible 1 (PIC1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4558"
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37.00
100.00%
100.00%
11.82%
                                                                                                                                                                                     GI:9856099
Gingle, A.,
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Matches:
Conservative:
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Indels:
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d 1 (PI1)
  Dean, R.,
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37
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) Sorçhum
    Sudman, M. and Pratt
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                                                                                                                                                                                                                                                     EST 18-AUG-2000
bicolor cDNA,
                                                                      Tracheophyta;
aceae; PACC
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BE366914
LOCUS
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Best Local Similarity:
Query Match:
DB:
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                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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JOURNAL
                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                          sorghum.
Sorghum bicolor
                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                      EST
Contact: Cordonnier-Pratt MM
                        Unpublished (2000)
                                                                           Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and
                                                                                                                                                                                                                                                        BE366914.1
                                                                                                                                                                                                                                                                              BE366914
                                                                                                                                                                                                                                                                                                mRNA sequence.
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                                     An EST database from Sorghum: pathogen-induced
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Tel: 706 542 1860
Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
                                                                                                 ade; Panicoideae; Andropogoneae; (bases 1 to 480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: JEN REV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cultivar) were infected with pathogen (isolate FRM42] of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Anthracnose-infected leaves from two-week-old sorghum plants 48 hr after inoculation; vector: pBluescript II from Lambda Zap II; Site_1: X Site_2: EcoR; Two-week-old sorghum plants (823 Site_2: EcoR; Two-week-old sorghum plants)
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/db_xref="taxon:4558"
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165 c
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Matches:
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Indels:
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                                                                                                                         Sorghum.
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1 (PI1) Sorghum bicolor cDNA,
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FEATURES
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AUTHORS
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ORGANISM
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BE600167
COMMENT
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Best Local Similarity:
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                                                                                                                                                                                                                                                                        488
PI1_80_B04.b1_A002 Pathogen
mRNA sequence.
              An EST database from Sorghum: Unpublished (2000)
                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                 EST
                                                                       Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                  BE600167.1 GI:9855240
                                                                                                                                                                                                                                                         BE600167
                                                                                                                                                                     Sorghum bicolor
                                                                                                                                                                                               sorghum
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 706 542 1860 Fax: 706 583 0210
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                                                                                            (bases 1 to 480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          two-week-old Sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42] of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate STS deriving from
the pathogen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Pathogen induced_1 (PI1)"
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37.00
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Matches:
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Mismatches:
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                                 pathogen-induced plants
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                                                                       Dean, R., Sudman, M.
                                                                                                                                                                                                                                                                                                                  ∏RNA
                                                                                                                                                                                                                                                                                           mRNA linear EST 18-AUG-2000
1 (PI1) Sorghum bicolor cDNA,
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Query Match:
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                                                                                        REFERENCE
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                        TITLE
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                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
                                                                                                                                                                                                                                                                                                                                                                                                                                          72 AspGlySerIleLeuLeuAspAlaGlyGlyGluLysThrAlaGlyProAsn 88
                                                                                                                                                                                                                                                                                                                                                                                                                    GACGGCTCGATCCTTCTCGACGCCGGAGGGGGAGAAGACGGCAGGCCCCAAC
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Sequences have been trimmed
below Phred quality 16. The
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The University of Georgia, Department of P.
An EST database from Sorghum: pathogen-induced plants unpublished (2000)
                                                                                                                                                                                                                                                               mRNA sequence.
BE599526
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PI1_88_F01.b1_A002 Pathogen
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                                                               1 (bases 1 to 487)
Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                         Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-Torgan: Anthracinose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation:
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45.
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda Zap II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
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/db_xref="taxon:4558"
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RESULT 14
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                                                           AUTHORS
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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                                                                                    Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 495)
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An', L
                                                     Cordonnier-Pratt, M.-M., Gingle, A.,
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/clone_lib="pathogen induced 1 (PI1)"
/clone_lib="pathogen induced 1 (PI1)"
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/db_xref="taxon:4558"
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Contact: Cordonnier-Pratt MM
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PI1_32_E10.b2_A002 Pathogen i
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                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poclade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 522)
                                                                                                      Sorghum bicolor
Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
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/note="Organ: Anthracnose infected leaves from
/note="Organ: Anthracnose infected leaves from
/note="Organ: Anthracnose infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860
Fax: 706 583 0210
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
Site_2: EcoRI; Two-week-old sorghum plants esuptum isolate).

RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: while
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
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-DB=EST -QFMT-fastap -SUFFIX-rst -MINMATCH-0.11 -LOOPCL-0 -LOOPEXT=0
-UNITS-bits -START-1 -END--1 -MARIX-blosum62 -TRANS-human40.cdi -LIST-45
-DCCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTEMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US10047825_eCGN_1_1_1456_eTNAT_26042003_111958_7143 -NCPU-6 -TCPU-3
-NO_MAR -LARCEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXI-0.5 -FGAPOP-6 -FGAPEXI-7
-YGAPOP-10 -YGAPEXI-0.5 -DELEDP-6 -DELEXI-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	ACCESSION	RESULT I AA979912 LOCUS DEFINITION		45	Δ.Δ. Δ.Δ.	4⊥ 42	40	ມ ພ 80 90						200				22 23 7	21	19 20	18	16 17	15	113 14	12	110 8		8		4. 4. 9	ωι	1 9	Result No. S
Eukaryota; Viridiplantae; Streptophyt- Spermatophyta; Magnoliophyta; Liliops clade; Panicoideae; Andropogoneae; Ze 1 (bases 1 to 848) Wen, T.J., Ashlock, D.A. and Schnable, P	_	AAS AAS	AAS		700	703.5	705	708	718.5 716		724 5	736	739.5			749	750	76	76 67.	771	781 774	782	788	793	793	822	4⊥ 83	871	89	904.5	28.	942	99.	core
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ida; Poales; Pa.	a: Embryophyta:		mRNA linear EST 26-MAY-1998 cDNA clone MEST3-D6 5', mRNA		PI1_94_	NO.	HV_CEaC	BQ165051 EST610920	BG442996 GAEa001 · AV9:25367 AV925367	BE555297 Sp87906.y	. BM359358 GA Ea001	BE594365 PI1_32_E1	BQ164905 EST610774	BE597461 PI1_69_G0	BE595535 PII_56_H0	AY109094 Zea mays . BE034991 MM01A12 M	BQ744368 WHE4114_G	BF267871 HV_CEa001	BE600823 PI1_90_F0 AY105520 Zea mays	BE357554 DG1_21_H1	BE366224 PII_31_AU BE125306 DG1 18 A1	PI1		DG1		Zea	HV_		3 2	EM1	38	Zea	79912 MEST3-D6.	Description

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BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3
Plate: MEST3 row: D column: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schnable laboratory
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Contact: Schnable,
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(515)-294-0975
(515)-294-2299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: green seedlings; Vector: pAD-GA14; Site_1: ECORI; Site_2: XhoI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA POII-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZAP lambda vector (Stratagene) and excised as pAD-GA14 phagemids."
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/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
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/clone="MEST3-D6"
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/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The University of Georgia, De Plant Sciences Building, Rm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 576
                                                                                                                                                                                                 /db_xref="taxon:4558"
/clone_lib=Light Grown 1 (LG1)"
/clone_lib=Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: xhoI; Site_2: EcoRI
: The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sorghum bicolor"
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                    Conservative: Mismatches: Indels:
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Department of Plant Biology
m. 2502, Athens, GA 30602-7271, USA
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Matches:
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                                                                                                                                              Unpublished
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    Morgante,M. and Tingey,S.V.
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                       uArgGlnGlnThrCysProArg-----SerGlyGlyAspGlyAsnLeuAlaProIleAs
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/db_xref="taxon:4577"
/clone="PCO104850"
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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Sequences have been trimmed
below Phred quality 16. The
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Contact: Cordonnier-Pratt MM
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Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and An EST database from Sorghum: developing embryos
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/note-"Organ: Embryos germinated for 24 hr; Vector:
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ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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                                                                                                                                                                                                                                                    ATCAAGACCAACGTGGAGGCCGCGTGCCCCGGCGTCGTGTCGTGCGCCGACATCCTTGCC
                                                                                                                                                                                                                                                                                    ACNGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCCGGTGCACCACCTTCCGC
                                              sequence.
BG462797
BG462797.1
EST.
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 591)
                                                                               BG462797
EM1_45_F11.b1_A002
                                        sorghum
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/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Eco
: The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

23 c 188 g 110 t 2 others
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914.00
93.94%
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56.98%
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(EM1)
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US-10-047-825-4 (1-313) x BG462797
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Best Local Similarity:
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ThrCysProArgSerGlyGlyAspGlyAsnLeuAlaProIleAspValGlnThrProVal
                                                                        GlyArgIleTyrGlyAspThrAspIleAsnAlaSerPhe---AlaAlaLeuArgGlnGln
                                                                                                                              GACATGACGGCGCTGTCGGGCGCGCACACCATCGGGCAGGCCCGGTGCACCACCTTCCGC
                                                                                                                                               AspMetThrAlaLeuSerGlyAlaHisThrIleGlyGlnAlaArgCysThrThrPheArg
                                                                                                                                                                                                  TCGACGGCGAGCCTGGGTACGCTCATCTCGCTGTTCAGCAGGCCAGGGCCTGTCGGCGCGC
                                                                                                                                                                                                                       ProThrAlaSerLeuGlyThrLeuIleSerLeuPheGlyArgGlnGlyLeuSerProArg
                                                                                                                                                                                                                                                                                                                                                CTTGCCCTTGCCGCGAGACGGAACCAATCTGCTCGGCGGGCCGACCTGGAACGTGCCG
                                                       Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA
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Sequences have been trimmed
below Phred quality 16. The
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/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Si
EcoRI; The library was made from poly-A RNA in the
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
214 c 190 g 87 t
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/db_xref="taxon:4558"
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30602-7271,
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US-10-047-825-4 (1-313) x BE362200 (1-593)
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                                                                         ArgAlaAlaMetThrGlnAlaValAlaSerGluGlnArgMetGlyAlaSerLeuLeuArg
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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Sequences have been trimmed to exclude
below Phred quality 16. The threshold f
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1 (bases 1 to 593)
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/db_xref="taxon:4588"
/db_xref="taxon:4588"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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                                                                                                                                                                                                                                                                          Seq primer: JEN REV High quality sequence stop: 531 POLYA-No.
                                                                                                                                                                                                                                                                                                                                            Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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BE362356
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Contact: Cordonnier-Pratt MM
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DG1_86_C05.b1_A002 Dark
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                                                                                            /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: Dark-grown seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 210 c 181 g 105 t
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                                                                                 L.H. An EST database from Sorghum: Unpublished (2000)
Contact: Cordonnier-Pratt MM
Contact: for Genomics and B
                                                                                                                                                                           Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poacles; Poaceae; PACC
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DG1_81_G11.b1_A002
                                                          Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                        clade; Panicoideae; Andropogoneae;
1 (bases 1 to 615)
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Sequences have been below Phred quality
                                                                                                                                             Cordonnier-Pratt, M.-M.,
                       Email: mmpratt@uga.edu
                                    706 542 1860
706 583 0210
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/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EccRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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/db_xref="taxon:4558"
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AlaGlyProAsnLeuAsn---SerValArgGlyPheGluValIleAspThrIleLysArg
                                                                                                                                                                                                                     GTGGTCCACCAGGGCTGCGACGCGTCCATTCTGCTGAACGACACGTCCGGGGAGCAGACC
                                                                                                  ATTAGCACGTCGTATATGCATGCGATTAATTAACCAGGAGGCATCATGGTGAAATTTCTG
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Zea mays
Eukaryota;
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Submitted (25-APR-2002) Maize
Missouri, Columbia, MO 65211,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1570)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
Overgo Probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
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                                                             -GlnGlyCysAspGlySerIleLeuLeu---AspAlaGlyGlyGluLysThr
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/db_xref="MaizeDB:634070"
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                                                                                           i (bases 1 to 829)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resofter barley genomics: Blumeria infected incompatible (Mla13) seedling leaf CDNA library
                 Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                           Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
                                                  Contact: Wing RA
                                                                 On Nov 17, 2000 this sequence version
                                                                                  Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                BF263468 829 bp mRNA linear EST 23-OCT HV_CEa0006N05f Hordeum vulgare seedling green leaf EST-library HVCDNA0004 (Blumeria challenged) Hordeum vulgare cDNA clone
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 Hall,
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29634, USA
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a; Poales; Poaceae; Pooideae
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GACGGGTCCATTCTCTTGGATGACGTGGGTAGCTTCGTGGGCGAGAAGACGGCCCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CIGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             green seedlings were challenged with isolate A27 (AvrMlal3) of Blumeria graminis f. sp. horded, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of fall three RNA pools were combined, poly(A) RNA was purified from the mixture, one CDNA library was made, and I million pfu were in vito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
a 293 c 250 g 139 t
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http://www.genome.clemson.edu/projects/barley.
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/clone=lib="Hordeum vulgare seedling green leaf EST
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/tissue_type="seedling green leaf"
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACAGTCTATGGTGAATATGGGAAACATCTCGCCACTGACAGGGTCACAAGGTGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, Tel: 706 542 1860 Fax: 706 583 0210 Email: mmrrr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mmpratteuga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sorghum.
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE597430.1
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                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop:
                                                                                                                                                                                                                 /clone_lib="Pathogen induced 1 (PII)"
/clone_lib="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (Lsolate FRW42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda Zap HI. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
                                                                                                                                                           a
                                                                                                                                                       the pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
2.31e-73
809.00
93.30%
89.39%
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Percent Similarity: Best Local Similarity:

Conservative: Mismatches:

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RESULT 14
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    FEATURES
                                                                                                                                                             TITLE
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                                                                                                     Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                              clade; Panicoideae; Andropogoneae;
1 (bases 1 to 561)
Cordonnier-Pratt, M.-M., Gingle, A.,
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DG1_82_H08.b1_A002 Dark
                        High
                                  Seq
                                                    Email: mmpratt@uga.edu
Sequences have been tr
below Phred quality 16
                                                                                                                                        Contact: Cordonnier-Pratt MM
                                                                                                                                                An EST database from Sorghum: dark-grown seedlings Unpublished (2000)
                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
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BE361738
             High quality sequence POLYA=No.
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           AUTHORS
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Cordonnier-Pratt, M.-M.,
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                                                                      sorghum
                                                                                                               sequence
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US-10-047-825-4 (1-313) x BE361738 (1-561)
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              Sorghum bicolor

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 570)
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DG1_30_A01.b1_A002
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/db_xref="taxon:458"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap-grown seedlings; Vector: Lam
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                                                        CGGCGGGACTCGACGGCGAGCGCGTCCCTTGCCAACAGCAACCTCCCGCAGTCGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An EST database from Sorghum: dark-grown seedlings Unpublished (2000)
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Seq primer: JEN REV
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/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-a RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
198 c 167 g 110 t
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/db_xref="taxon:4558"
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